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6, 2005, 14:16:48; Search time 43 Seconds (without alignments) 443.045 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                     OM protein - protein search, using sw model
                                                                                                                                    April
                                                                                                                                       Run on:
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1025 1 GICARVDASFQPQGSLAPTA......FLREIRTIASDPDERFFINV 198 US-09-647-544-2_COPY_140_337 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

100665 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 198

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir2:* 4: pir4:* PIR_79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descri	ιρ	in	hypothetical prote		4	hypothetical prote		Ç	conserved hypothet	hypothetical prote	acetyltransferase,	hypothetical prote	_	14	$\overline{}$		30S ribosomal prot	acetyl transferase	virulence regulato	conserved hypothet	Ni, Fe-Hydrogenase	gonadoliberin II p	1	hypothetical prote	O)	hypothetical prote		U	IS 426 transposase
SUMMARIES	Д	147230	151310	E75293	B71454	I61890	E85068	AF0860	AE3363	A98075	C70686	G95210	H75017	AF2520	E75544	H81150	A69201	D83114	F86723	A82674	D83636	F71089	RHID2S	137024	F98333	AD2949	H84412	837713 .	AF3122	AG3158
	DB	. ~	~	~	~	~	~	~	~	~	7	7	~	7	7	7	7	7	7	~	7	~	-	N	~	~	~	~	~	7
	ength		194	164	169	170	197	118	188	148	129	148	171	151	193	181	197	166	187	138	180	147	98	170	189	196	190	129	129	129
٠		. 6	7.2	6.9	6.9	6.9	6.9	6.9	6.8	6.8	6.7	6.7	9.9	9.9	9.9		6.5	6.5	6.5	6.4	6.4	6.4	6.3	6.3	6.3	6.3	6.3		6.2	6.2
	r F	336	74	71	71	71	71	70.5	70	69.5	69	68.5	68	67.5	67.5	67	67	99	99	99	99	65.5	65	65	65	65	64.5	64	64	64
	Result No.	-	8	e	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

beta 8 integrin - chicken (fragment)

beta 8 integrin - chicken)

c;Species: Gallus gallus (chicken)

c;Date: 0.4-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

c;Accession: 151310

R;Venstrom, K.; Reichardt, L.

Mol. Biol. Cell 6, 419-411, 1995

A;Reference number: 151310; MUID:95352850; PMID:7542940

A;Reference number: 151310; MUID:95352850; PMID:7542940

A;Accession: 151310

A;Accession: 151310

A;Accession: 151310

A;Accession: 151310

A;Accession: 151310

C;Superfamily: integrin beta chain; laminin-type EGF-like homology

paralytic peptide	hypothetical prote	gonadoliberin II p	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	hemoglobin VIIB-6	hemoglobin VIIB-8	hypothetical prote	hypothetical prote	hypothetical prote	sulfur-regulated p	hypothetical prote	hemoglobin VIIB-5/	hemoglobin VIIB-5
JC7739	T30772	A53453	AH1330	H89940	B75029	AH1701	A30477	S04499	T32808	F84286	D83623	B56274	D84397	JT0292	JT0349
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13	15	ω	Н	ä	ä	H	16	16	19	16	180	18	10	16	Ä
••	• •						•			•			6.0 10		
6.2	6.2	6.2		6.1	6.1	6.1	•	0.9	0.9	0.9	0.9	0.9	•	0.9	

ALIGNMENTS

RESULT 1 147230

VLA-2 I N;Alter C;Speci	VIA-2 protein - pig (fragment) N;Alternate names: glycoprotein Ia/IIa C;Species: Sus scrofa domestica (domestic pig)
C;Date: C;Acces	C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004 C;Accession: 147230; S21518
R; Bahou	R;Bahou, W.F.; Potter, C.L.; Mirza, H.
A;Title	blood w., 3/34/3/41, 1934 A:Title: The VLA-2 (alpha 2 beta 1) I domain functions as a ligand-specific recognition
A;Refer	A;Reference number: 147230; MUID:95036279; PMID:7949129
A; Acces	A; Accession: 147230
A;Statt	Ak)stetus: preliminary; translated from GB/EMBL/DDBJ a.malegale tymes menn
A. Resid	A. Residues: 1-191 - BAH>
A, Cross	A, Cross-references: UNIPROT: Q29124; EMBL: Z12137; NID: 92158; PIDN: CAA78125.1; PID: 92159
C; Keywc	C;Keywords: glycoprotein
Query	Query Match 32.8%; Score 336; DB 2; Length 191;
Match	DOCAL SIMILATING 19:57; FIGU. NO. 1:56-25; Indels 0; Gaps 0;
ò	42 WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFRTKEBVVRAAKNLSRREG 101
qq	
δλ	102 RETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVVTDGESHDGEELPAALKACEAGRVTRY 161
Ор	61 DLINTFKAIQYARDSAYSAAAGGRPGATKVMVVVTDGESHDGSMLKAVIDQCNNDNILRF 120
'n	162 GIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
쉽	:

2; Length 169;

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6.9%; Score 71; DB ilarity 25.7%; Pred. No. 34; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 KASAGLLGAHAAAITAYALTL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: alpha-2-macroglobulin
                                                                                                                                                                                                                                                                                                                                 FRSE--EELLHVLEKC 167
                                                                                                                                                                                                                                                                                                   138 GESHDGEELPAALKAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 22/2; 74/3; 113/3
Query Match
Best Local Similarity
Matches 35; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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B71454
hypothetical protein PH0289 - Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: B71454
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A7100; MUID:98344137; PMID:9679194
A;Reference number: A7100; MUID:98344137; PMID:9679194
A;Retus: preliminary; nucleic acid sequence not shown; translation not shown
A;Roseluce: Lifes <ARAN
A;References: UNIPROT:OS8027; GB:AP000001; NID:9325128; PIDN:BAA29361.1; PID:9325
A;Retus: preliminary surce: strain OT3
A;Nobe: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75293 J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome, sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-164 <MHI>
A;Residues: 1-164 <MHI>
A;Cross-references: UNIPROT:Q9R846; GB:AE002060; GB:AE000513; NID:g6460082; PIDN:AAF1183
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A/Reference number: A75250; MUID:20036896; PMID:10567266
                                                       'n
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                                                                                                75 VHEWSLGD----FRIKEEVVRAAKNLSRREGREIKTAQAIMVACTEGFSQSH-GGRPEAA 129
                                                                                                                                 82 -- DFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 TAEGRIKKDAERLAAELALRE-LDGSDAPPVPAAPATPIAQQSEPWPIYAQVLAEAVBAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 SRTLÝPMNAKGDLIARLV-----SLGLGTPTFEAEAHGPAHERTFHVKVWSSGQVIA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 SNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQY---GESPVHE-----WSLG----
                                                       Gaps
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                                                       12;
     DB 2; Length 194;
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                                                     27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.9%; Score 71; DB 25.2%; Pred. No. 33; tive 19; Mismatches
                           Pred. No. 21;
7; Mismatches
  ch 7.2%; Score 74; 1 Similarity 36.1%; Pred. No. 326; Conservative 7; Mismatch
                                                                                                                                                                                                130 RLLVVVTDGESH 141
                                                                                                                                                                                                                                           120 RLLLVMTDQTSH 131
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Best Local Similarity
Matches 38; Conserva
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  Query Match
Best Local S
Matches 26
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A,Gene: DR2281
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C;Accession: I61890
R;Kawaguchi, H.; Zaleska-Rucczynska, Z.; Figueroa, F.; O'hUigin, C.; Klein, J.
mmunogenetics 35, 16-23, 1992
A;Title: C4 genes of the chimpanzee, gorilla, and orang-utan: evidence for extensive home A;Reference number: I37023; MUID:92104634; PMID:1729169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Accession: E85068
R; anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Marure 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID: 20083488; PMID: 10617198
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    9
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                                                                                                                                                                                                                                                                                                    102 LRDIDETRENLLRALKELEHEKGSEVEEIKKKKLEIALK-----RNEVARKLLTLIMQ 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 PVIHRGMQGGLVGNDETVALTAFVTIALHHGLAVFQDEGAEPLKQRVEASISKANSFLGE 126
                                                                                                                                                            52 YSLSHVSSAMRVLEG-----VGLVQRVKKPGDRKAYFIATKNFSEWRSSAFYEKI 101
                                                                                                                                                                                                                                                 ----RTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAAR-LLVVVVTD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AT4905450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement C4 - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
                                                                                ----VHEWSLGDF----
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: AT4g05450
A;Map poaltion: 4
C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
C;Keywords: 2Fe-2S; metalloprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 170;
Indels
    45;
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A;Molecule type: DNA
                                                                                40 YPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 23.4%; Pred. No. 34;
Matches 33; Conservative 19; Mismatches
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A;Cross-references: UNIPROT:Q8DNN2; GB:AE007317; PIDN:AAL00430.1; PID:g15459297; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.H.; Jaskunas, S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Mycobacterium tuberculosis (Species: Mycobacterium tuberculosis) (Species: Mycobacterium tuberculosis) (Species: Mycobacterium tuberculosis) (Species: Mycobacterium tuberculosis) (Spacesion: 70686 (S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical protein spr1627 [imported] - Streptococcus pneumoniae (strai) c) Species: Streptococcus pneumoniae C) Accession: A98075 [S. Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A,Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A,Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                           SEKILRAATELAQEVGPAHISLDA--VAARAGLSK--GGLLYSFPTKAKLLEAMVEKYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 POGSLAPTAQR-----CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQ
        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EQIQVGL------VQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKQEQGLGSQALRKFVSLAFENEDIDSISLNVF----EANQRAQNLYQKEGFE 130
                                                                                                                                                                                                                                                                                                                      141 HDGEELPAALKACEAGRVTRYGIAVLGHY-LRRQRDPSSFLREIRTIASDPD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
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        10;
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        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 69.5; DE
25.7%; Pred. No. 40;
Live 23; Mismatches
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        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>..</u>
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Best Local Similarity 25...,
Local 29; Conservative 2
        Conservative
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A;Molecule type: DNA
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        28;
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        Matches
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C;Date: 0.1Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3363
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Acid, Sci. U.S.A. 99, 443-448, 2002
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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Almonella enterica subsp. enterica serovar Typni
C.Species: Salmonella enterica subsp. enterica serovar Typni
A,Note: this species has also been called Salmonella typni
A,Note: this species has also been called Salmonella typni
C,Accession.
A,Baccession.
A,Baccession.
A,Baccession.
A,Authors: P.
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.)
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.)
A,Reference number: AB0502; MUID:21534947; PMID:11677608
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A;Cross-references: UNIPROT:Q8YHB1; UNIPROT:Q8G0K2; GB:AE008917; PIDN:AAL52072.1; PID:g1
F;118,124,127,165/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
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ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-118 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06069.1; PID:g16504035; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                      29 KNLHRSYGHYLQSLPVVPRQARTSQEAWFLKSHKFCTSSTTSSENGDEETEKITIIFVD- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                      139 ESHDGEELPAALK------ACEAGRV--TRYGIAVLGHYLRRQRDPS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KDGEEIPVKVPIGMSVLEAAHENDIDLEGACEASLACSTCHVIVMDTBYYNKLEEPT 144
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-----WEKDAFLRKVKTGMIKPDE 109
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                                                                                         DB 2; Length 197;
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                                                                                                                                                                          39; Indels
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Pred. No. 48;
                                                                                     6.9%; Score 71; DB 22.7%; Pred. No. 41; ive 15; Mismatches
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                                                                            Query Match
Best Local Similarity 22.7
Matches 27; Conservative
                                                                                                                                                                                                                                                                94 KNLSRREG-----
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Best Local Similarity
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A;Gene: BMEI0891
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Best Local Si
Matches 24,
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Db 17 PAGAAVARRIRGETVHAPAHFDVEVIGAIRQAVVRQLISDHEGL 60	Qy 84RTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAAR-LLVVVTD 137
Qy 65 VGLVQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQS 121	Db 102 LRDIDETKESIMRALEELEGEGGGSEVEEIKEKLKMALRRNEVARKLLTLIMQ 153
Db 61 VVVVNFLSLPVRRWPLKPFTQRAYQLRSTHTVADGAYVALABGLGVPLITCDGRLAQS 118	Qy 138 GESHDGEELPAALKAC 153
Oy 122 HGGRPB 127	Db 154 FKSEBELLKVLESC 167
Db 119 HGHNAE 124	t mattered
RESULT 11	AESOLI 13 AFS250 hypothetical protein alr7342 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al]
acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae	Vigetter Nostoc 8p. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
	C;Accession: AF2220 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Uakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nictualing n.; Margan, A.E.; Faulsen, 1.1.; Elsen, O.A.; Read, 1.D.; Fereston, S.; Reidon, O., J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B.	NAKAZAKI, N.; SIMIMPO, S.; SUGIMOCO, M.; Takazawa, M.; Tamada, M.; Tabuda, M.; Tabada, S. DISTA, S. B. 205-213, S. 20101 B.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
Science 233, 498-506, 2001 A; Authors: Loftus B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, B.H.le. Complete Ganger Sequence of a virulant isolate of createness meaning and	A.Reference number: AB1807; MUID:21595285; PMID:11759840 A.Accession: AR252.0 A.Gratus: ovelimitato
	A.Molecule type: DNA A.Residues: 1-151 <kur></kur>
A;Status: preliminary A;Molecule type: DNA b:Deciding 1,140 Vm	A;Cross-references: UNIPROT:QBYKF6; GB:BA000020; PIDN:BAB77100.1; PID:g17134541; GSPDB:G! A;Experimental source: strain PCC 7120
A) resetuces: 1.1-19 CNUR. A). A). COSE-references: UNIPROT:097P37; GB:AE005672; PIDN:AAK75880.1; PID:914973306; GSPDB:GA; Experimental source: strain TIGR4	Vicene: alr'1342 A'Genoe: plasmid
C;Genetics: A;Gene: SP1807	Query Match 6.6%; Score 67.5; DB 2; Length 151;
Query Match 6.7%; Score 68.5; DB 2; Length 148;	Similarity 4; Conservat
28; Conservative 25; Mi	PEQIQUGLUQYGESPVH-EWSLGDFRTKEEVVRAAKNLS
9 SPQPQGSLAPTAQRCPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDP	Db 95 KRLVAEVFVNNRSVNLTMVQEQQAVVYRQYLKGYTNTKEQFLQAEANAKQOK 146
DD 27 SFQEQW-MGPRIP-FLLTLQALEGVFSIFDEQEFVGFIQKIRLEDSNLHIGRFFINP 81	RESULT 14
Qy 61 BQIQVGLVQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRE 103 :::	E75544 Jag-related protein - Deinococcus radiodurans (strain R1) C.Species: Deinococcus radiodurans C.Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 09-Jul-2004
. 12	C; Accession: E75544 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; J
H/501/ hypothetical protein PAB1243 - Pyrococcus abyssi (strain Orsay) C.Sbecies: Pyrococcus abyssi	, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, D.; Utterback, T.; Zalewski, C.; Mal S.; Suith, H.O.; Venter, J.C.; Fraser, C.M. Science 286. 1571-1577. 1999
e_revision 20-Aug-1999 #text_change 09-Jul-2004	A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A, Reference number: A75250, MUID:20036896, PMID:10567266
Library, July 1999 abyssi genome sequence: insights into archaeal chromosome stru	A.Accession: E75544 A.Status: preliminary A.Molecule type: DNA
A; McTerence number: A: 5001 A; Accession: H75017 A; Attacus: preliminary A; Molecule type: DNA	Ajrosiude: 1-153 mni> Ajrosi-references: UNIPROT:Q9RXR1; GB:AE001886; GB:AE000513; NID:g6457921; PIDN:AAF09828. A;Experimental source: strain R1 C;Genetics:
L «KAW» 1 «KAW» 2	A;Gene: DR0246 A;Map position: 1
Ajanetimental Bource: Briain Orbay C/Genetics: Ajgene: PAB1243	Query Match 6.6%; Score 67.5; DB 2; Length 193; Best Local Similarity 24.5%; Pred. No. 84; Matches 40; Conservative 22; Mismatches 50; Indels 51; Gaps 9;
Query Match 6.6%; Score 68; DB 2; Length 171; Best Local Similarity 24.3%; Pred. No. 65; Matches 33; Conservative 17; Mismatches 44; Indels 42; Gaps 6;	13 QGSLAPTAQRCPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPE-QIQVGLVQYG 71 ::
YPWSEVQTFLRRLVGKLPIDPEQIQVGLVQYGESPVHEWSLGDF	72 ESPVHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSCGHGGRPE-
DD 52 ISTSHISSAMKVEGGVGEVQKIKKFGDKKAIFVAIKNFSEWKSSAFIEKI IOI	Db 69RETEDALEAEISGENAARLAGRDGRTLGAISVIAYAVLAK-HAGRGDL 115

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RESULT 15
Hall50
hypotetical protein NMBO861 [imported] - Neisseria meningitidis (strain MC58 serogroup C,Species: Neisseria meningitidis
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C,Accession: H8150; P61872.
R,Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; T.J. H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 200.
A,Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A,Title: Complete genome sequence of Neisseria meningitidis serogroup B strain,MC58.
A,Accession: H81150
A,Scatus: preliminary
A,Accession: H81150
A,Scatus: preliminary
A,Residues: 1-181 <-TET>
A,Cross-references: UNIPROT:Q9JR36; GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF4127
A,Esperimental source: serogroup B, strain MC58
A,Experimental source: serogroup B, strain MC58
A,Experimental source: serogroup B, strain MC58
A,Experimental source: serogroup B, strain of Neisseria menigitidis Z2491.
A,Reference number: Asignales, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A,Reference number: Asignales of a serogroup A strain of Neisseria menigitidis Z2491.
A,Recession: P18172.
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A/Molecule type: DNA
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A/Residues: 1-181 <PAR>
A/Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84336.1; PID:g737976
A/Experimental source: serogroup A, strain 22491
C/Genetics:
A/Gene: NMB0861; NMA1073
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128 ------AARLLV-VVTDGESHDGEELPAA 149
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Machino sequence (i.i., Mirza H.;
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Trecognition sequence for endothelial cell attachment and spreading:
The VLA-2 (alpha 2 beta 1) I domain functions as a ligand-specific
Trecognition sequence for endothelial cell attachment and spreading:
The VLA-2 (alpha 2 beta 1) I domain function.";
Blood 84:3734-3741(1994).
REMBL; Z12137; CAA78125.1; -.
REMBL; Z12137; CAA78125.1; -.
REMBL; Z12137; VWA, 1.
REMBL; SPRO0923; VWA, 1.
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QBMVP6
QBYHB1
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70 YGESPVHEWSLGDFRTKEEVVRAAKNLSRRE--GRETKTAQAIMVACTEGFSOSHGGRPE 127
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                                     14 FVEEVIRRMDVGQDGIHVTVLQYSYVVTVEHSFREPQSKDVVLQRLREVRYRGGNQTNTG 73
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MEDLINE=22248966; PubMed=12361966;

Davidson B.J., Swalla B.J.;

"A molecular analysis of ascidian metamorphosis reveals activation of an innate immune response.";

Development 1129-4733-4712 (2002).

EMBL: AF483028; AAM76108.1.;
                                                                     108 QAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDG-EELPAALKACEAG 156
                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 9.0%; Score 92; DB 2; Length 146; Local Similarity 23.9%; Pred. No. 3.1; hes 32; Conservative 29; Mismatches 49; Indels
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Doerig C.D., Doerig C.M.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X87840; CAA61109.1; -.
InterPro; IFR002035; VWF_A.
Pfam; PF00092; VWA; 1.
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Stolidobranchia; Pyuridae; Boltenia.
NCBI_TaxID=63515;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Collagen-like protein 3 (Fragment).
                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Thrombospondin-related anonymous protein (Fragment)
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122 APKVTILFTDGNEN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AARLLVVVTDGESH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boltenia villoga.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=3D7;
                                                                                                                                                                                                                                                                                Name=TRAP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=vwa3;
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Matches
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Q8MVN3
                                                                                                                                                    RESULT 4
096930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 LFIDPEQIQVGLVQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 EGFSQSHGGRPBAARLLVVVTDGESHDGEELPAALKACEAGRVTRYGIAVLGHYLRRQRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 YAYSAASGGRESATKVWVVVTDGESHDGSMLKAVIDQCNHDNILRFGIAVLGYLNRNALD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LDIGPTKTQVGLIQYANNPRVVFNLNTYKTKBEMIVATSQTSQYGGDLTNTFGALQYARK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                               Homo sapie,s (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos
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10.1%; Score 103.5; DB 2; Length 143;
Best Local Similarity 23.6%; Pred. No. 0.29;
Matches 26; Conservative 27; Mismatches 56; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
29.2%; Score 299; DB 2; Length 156;
Best Local Similarity 44.1%; Pred. No. 1.5e-18;
Matches 63; Conservative 24; Mismatches 56; Indels
                                                                                                                                                                                                                                           GO; GO:0007229; P:integrin-mediated signaling pathway; IEA, InterPro; IPR002035; VWF_A. InterPro; IPR00921; VWA; 1. PRINTS; PR00453; VWADOMAIN. SMART; SM00327; VWA; 1. PROSITE; PS50234; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF004285; AAB61376.1; -..
InterPro; IRR02035; VWP.A.
Ffam; PF00092; VWA; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                          Kunicki T.J., Kritzik M.R.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF035968; AAC94975.1; --
HSSP; P17301; 1AOX.
                                                                                                                                                                                                                                                                                                                                                               1
156 156
156 AA; 17042 MW; BC7ABD63226C652B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 143
143 AA; 16099 MW; D472A917993E1C5A CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Von Willebrand Factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 PSSFLREIRTIASDPDERFFFNV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                  Integrin alpha 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
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24; Gaps

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144 -EELPAAL-KACEAG-----RVTRYGIA----VLGHY
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                                                                                                                                                                 STATE THE PRESENCE OF COURT AND DESCRIPTION OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                      18 PTAQR-CPTY--MDVVIVLDGSNSI--YPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGE 72
                                                                                                                                                                                                                                                                                                                                                                                 31 PCCSRPCPPYAVMDIVLVLDSSSSIGAENWLMLTDFVRGIINSFIVAEDAANFAIFRYNR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ANRNDSRRDSRKDRKKDDIEDQLVAINRITKVVKGGRRMRFAAVVIVGDRKGHVGFGTGK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 DVDVTTQILLNSYPGDIDGLTQAFGRIPYDGSGTFTGQGLGHALRVSLSPANGNRP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 --SPVHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Prittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Marcenler A., Klaenhammer T., Arigoni F., Schell M.A.; "The genome sequence of the problotic intestinal bacterium Lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
-I- SIMILARITY: Belongs to the ribosomal protein S5P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches 34; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.8%; Score 79.5; DB 2; Length 174; Best Local Similarity 32.0%; Pred. No. 50;
                                                                                                                                                                                                                                                         DB 2; Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE017201, AAS08342.1; -... GO; GO:0005622; C:intracellular; IEA. GO; GO:0015935; C:amall ribosomal subunit; IEA. GO; GO:0003735; F:structural constituent of ribosome; IEA. GO; GO:000412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                     19; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome, RIbonucleoprotein, Ribosomal protein. SEQUENCE 174 AA; 18717 MW; A922015D6183BA43 CRC64;
                                                                                                                                                                                  153
16666 MW; 3B02FA147CE5CB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 AA
                                                                                                                                                                                                                                                         7.9%; Score 80.5; I
25.0%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000851; Ribosomal SS.
InterPro; IPR005712; Ribosomal SS b/o.
InterPro; IPR005324; Ribosomal SS b/o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                 InterPro, IPR000436; Sushi_SCR_CCP.
InterPro, IPR02035; VWF_A.
Pfam, PF00092; VWA, 1.
PROSITE; PS50923; SUSHI; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Pfam; PF03719; Ribosomal S5 C; 1.
PIGTRAMA; TIGROLO21; rpsE bact; 1.
PROSITE; PS00885; RIBOSOWAL S5; 1.
PROSITE; PS50881; S5 DSRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30S ribosomal protein S5.
OrderedLocusNames=LJ0354;
Lactobacillus johnsonii.
                                                                                                                                                                                                                                                                                                        29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                  153 1
153 AA;
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                           Collagen.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                     PLALE TRANCE (1971):
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative invertase inhibitor precursor (Pollen allergen Pla a 1).
Platanus acerifolia (London plane tree).
Platanus acerifolia (London plane tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Proteales; Platanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 QGTCKKVAQRSPNVNYDFCVKSLGADPKSHTADLQGLGVISANLAIQHGSKIQTFIGRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 79.5; DB 1; Length 179;
24.8%; Pred. No. 51;
ive 25; Mismatches 39; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asturias J.A., Ibarrola I., Eraso E., Arilla M.C., Martinez A.; "The major Platanus acerifolia pollen allergen Pla a 1 has sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 24-35; 49-55; 61-71; 113-121 AND 151-158, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative invertase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pollen and stem, but not leaves.
-!- ALLERGEN: Causes an allergic reaction in human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
152B025E98879C5A CRC64;
62 AQEVPEAIRKAVEAGKKRMIKVPTVGTTIPHEVMGHY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology to invertase inhibitors.";
Clin. Exp. Allergy 33:978-985(2003).
-!- FUNCTION: Invertase inhibitor (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO06501; PME inhib.
InterPro; IPR004501; PME inhib.
Pfam; PF04043; PMEI; 1.
TIGREAMS; TIGRO1614; PME inhib; 1.
Allergen; Direct protein sequencing; Signal.
SIGNAL
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                                                                                                                                                                                       179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22744443; PubMed=12859456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AI -- MVACTEGFSQSHG 123
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179 AA; 19282 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=140101;
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Q6Z2B0;
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ID Q6
AC Q6
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194 1
194 AA;
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SEQUENCE 196 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9552850; PubMed=7542940;
A Venstrom K., Reichardt L.;
Tissum=10 an inferior mediate interactions of chick sensory neurons with
Theta 8 infegring mediate interactions of chick sensory neurons with
Taminin-1, collagen IV, and fibronectin.";
Mol. Biol. Cell 6:419-431(1995).
Mol. Biol. Cell 6:419-431(1995).
R Mol. Goldsoo, Libra.
R Mol. Goldsoo, Cell-matrix adhesion; IEA.
R Mol. Goldsoo, Cell-matrix adhesion; IEA.
R Mol. Goldsoo, Integrin.mediated signaling pathway; IEA.
R MART; SMO187; INB; INFERINB.
R MART; SMO187; INB; INB; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ICARVDASFQPQGSLAPTA-----QRCPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VAVRVQQLAVRVQQL--RAAHHVEIYNFSSTEELDRSVDRPQIMDSRNLSRRKQRARLEH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----rkeigg 34
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Gallus gallus (Chicken).
Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Gaps
                                                                                              P0467G09.7).
Mame=0J1034 COB.33; Synonyme=P0467G09.7;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OJ1034_C08.33 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Sasaki T., Matsumoto T., Yamamoto K.;
Susaki T., Matsumoto T., Yamamoto K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP0053831, BAD01379.1, -.
EMBL, AP004694; BAD01303.1; -.
                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 181 AA; 20089 MW; 9A2871CF7132993F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 KTAQAIMVACTEGFSQSHGGRPEAARLLVVVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTADG-----DERERSEEGRRQIAVRLAAVVS 119
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(TrEMBLrel. 27, Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
Beta 8 integrin (Fragment).
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                                                                                                                                                                                  75 VHEWSLGD----FRIKEEVVRAAKNLSRREGRETKIAQAIMVACTEGFSQSH-GGRPEAA 129
                                                                                                                                                                                                                                               67 IHVLSLTDNIAEFRNAVNKQKISGNIDTPEGGFDAMLQAAV-----CQSHIGWRKEAK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; APO05034; BAC70924.1; -..
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016118; P:electron transport; IEA.
InterPro; IPR000415; Nitroreductase.
Pfam; PF00881; Nitroreductase.
                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermithlis.
Bacteria, Actinobacteridae, Actinomycetales;
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
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                                         21847 MW; B845301262330547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA; 21419 MW; 0860C4DFF936CE39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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88.1%; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 AA
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01-07N-2003 (TrEMBLrel. 24, Last sequence) 01-07-2003 (TrEMBLrel. 25, Last annotate)
Putative nitroreductase family protein.
OrderedLocusNames=SAV3213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                      36.1%;
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                                                                                                                     26; Conservative
                                                                                                                                                                                                                                                                                                              130 RLLVVVTDGESH 141
                                                                                                                                                                                                                                                                                                                                                                     RLLLVMTDOTSH 131
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                                                                                            Best Local Similarity
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nes 36; Conserv
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NCBI_TaxID=272560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K96243
                                                                                                                                                                                                                                                                                                                                                                                    102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preisig-Muller R., Mederos y Schnitzler M., Derst C., Daut J., "Separation of cardiomyocytes and coronary endothelial cells for cell-specific RT-PCR.";
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                                                                                                                                                                       Von Willebrand factor (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preisig-Mueller R., Derst C., Mederos y Schnitzer M., Daut J.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF099069; AAD16289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proreobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative bacteriophage tail protein I.
ORFNames=BPSS1081;
                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                               134 AA
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                                                                                                            Created)
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MEDLINE=99345814; PubMed=10409222;
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Pfam; PP00092; VWA; 1.
PRINTS; PR00453; VWFADOWAIN.
PROSITE; PS50234; VWFA; 1.
                                                                                                       01-MAY-1999 (TrEMBLrel. 10,
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                                                             PRELIMINARY;
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PubMed=15377794;
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063LC8
1D Q63LC9
AC Q63LC
DT 25-OC
DT 25-OC
DT 25-OC
DF PLEAT
GN BULK
OC BUCK
OC BUC
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88 AVREVCASFGANVAMREWFEKTPKGRPGTFEILMTV---GARDG--IPATAEYVADIIAE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 VGKLFIDPEQIQVGLVQYGESPVHEWSLG----DF---RTKEEVVRAAKNLSRREG--- 101
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Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bascham I.R.,
Brooks K., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Chillingworth T., Cronin A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivilai S., Stevens K., Tunapa S., Vesararchavest M.,
Mnitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Mnitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Renomic plasticity of the causative agent of melicidosis,
Burkholderia pseudomallei ";
Proc. Nall. Acad. Sci. U.S.A. 101:14240-1425(2004).
REMBL; BX511965; CAH34140.1; -.
REMBL; BX511965; CAH34140.1; -.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M., Songaivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL, BX571966; CAH38648.1; - SEQUENCE 184 AA, 20280 MW; 4C81CE777D6078B2 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Matches 38; Conservative
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Sasaki T., Matsumoto T., Katayose Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
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MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
Beja O., SULXI M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMBL; AE008921; ALT. ALT. AESP, P43772; 10FH.

RESP, P606696; Treaponse core complex (sensu Eukaryota); IEA.

RESP, G0:0006417; P:protean folding; IEA.

RESP, G0:0006511; P:ubiquitin-dependent protein; IEA.

RESP, G0:0006511; P:ubiquitin-dependent protein catabolism; IEA.

RESP, RESP, PF0027; Proteasome, A.B.

RESP, RESP,
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0091C16.20 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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     143 VDRAKR-GTA---HY 153
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43; Conservative
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                                                                                                                                                                                                                                                            / Match 7.1%; Score 72.5; DB 2; Length 187; Local Similarity 26.0%; Pred. No. 2.3e+02; Indels 61; Gaps 63; Conservative 17; Mismatches 73; Indels 61; Gaps
Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                   EMBL; AP005820; BAD22464.1; -.
EMBL; AP004884; BAD21948.1; -.
Hypothetical protein.
SEQUENCE 187 AA; 20415 MW; 96A0FCC9628681DE CRC64;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 GICARVDASFQPQGSLAPTA......FLREIRTIASDPDERFFFNV 198 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 198

1433677

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Genesed 16Dec04:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:*geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp20048:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aau76862 Human int	Aau76853 Human int	Adr23227 Human int	Aau76863 Human int	Aau76854 Human int	Adr23228 Human int	Adr23225 Human int	Aae33535 Rat-human	Aae33537 Human alp	Aae33536 Rat alpha	Hum	Aau76860 Human int	Adr23226 Human int	Abp54908 Integrin		Aau76861 Human int	Aau09125 Human int	Aau19634 Human nov	Aau19794 Human nov	Human	Human	Human	Adc10976 Human pro	Aau19822 Human nov	Aau87675 Novel cen
COLUMNICO	ΩΙ	AAU76862	AAU76853	ADR23227	AAU76863	AAU76854	ADR23228	ADR23225	AAE33535	AAE33537	AAE33536	AAU76851	AAU76860	ADR23226	ABP54908	AAU76852	AAU76861	AAU09125	AAU19634	AAU19794	ABP47854	ABP48014	ADC10816	ADC10976	AAU19822	AAU87675
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de	Query	89.0	89.0	89.0	48.0	48.0	48.0	41.7	41.4	41.4	40.9	40.7	40.7	38.9	38.3	38.0	38.0		27.9		27.9		27.9		27.5	27.5
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	2 C C C C C C C C C C C C C C C C C C C	45

ALIGNMENTS

Human; integrin alpha subunit; A domain; Alpha 10; integrin beta subunit; A-like domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy; Human integrin alpha subunit Alpha 10 variant A domain. AAU76862 standard; protein; 195 AA (first entry) 21-MAY-2002 AAU76862; mutein. AAU76862

Homo sapiens. Synthetic.

Location/Qualifiers Key Misc-difference 193

/note= "Wild-type Ile substituted by any other amino acid" WO200209737-A1

07-FEB-2002.

31-JUL-2001; 2001WO-US023957.

31-JUL-2000; 2000US-0221950P. 11-JAN-2001; 2001US-00758493. 13-MAR-2001; 2001US-00805354.

(GEHO) GEN HOSPITAL CORP.

Li R, Xiong J; Arnaout AM,

WPI; 2002-188687/24.

Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.

Claim 53; Page; 55pp; English.

The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant

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                    CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 312 has been replaced by G or A at residue 312 have been replaced by C, or for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing a skeletal muscle injury, for treating disorders caused by ischaemia-tro purify variant integrin polypeptide ligands and parastic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents a human integrin alpha subunit Alpha 10 variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
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  integrin beta subunit A-like domain. The polypeptide, preferably the
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                                                                                                                                                                                                                                                                                                                                                                                                                                          89.0%; Score 912; DB 5; Length 195; 100.0%; Pred. No. 2e-96; 1.ve 0; Mismatches 0; Indels
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11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 195 AA;
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 313 and A at residue 320 have been replaced by C, or Or CD1b or for treating an inflammatory disorder, by contacting a test compound is a candidate compound for binding to CD1b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits a useful for reducing skeletal muscle injury, for treating disorders caused by ischaemian repertusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit Alpha 10 A domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.0%; Score 912; DB 5; Length 195; 100.0%; Pred. No. 2e-96; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human integrin alpha 10 subunit A domain.
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/label = A_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 195 AA;
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The present sequence is that of the human integrin alpha 10 subunit A domain. This includes an invariant Ile residue. The invention features contain integrin alpha subunit polypeptides in which the invariant Ile is substituted by Gly, Ala or some other amino acid (e.g. Val) or is deleted. The polypeptide can include part or all of the A domain. Seplacing the invariant Ile creates a variant integrin polypeptide that is southern to a variant integrin polypeptide that the wild type form of the subunit. Variant integrin polypeptides of the invention are useful in assays for compounds that integrin polypeptides of the invention are useful in assays for compounds integrin polypeptides of the invention are useful in assays for compounds of an integrin ligand to integrin, and for identifying activation. Specific ligands. They are also useful for generating antibodies, e.g. conocinal antibodies, which bind to the high efficiency form of an integrin some such antibodies recognise an epitope that is either not present or not accessible on an integrin that is in a lower affinity conformation. The invention also provides methods of administering a variant integrin polypeptide, or an antibody that selectivity binds it, to identify a ligand which binds to an active integrin. Such assays are useful for diagnosing inflammation, e.g. occult inflammation (e.g. useful for diagnosing inflammation, e.g. occult inflammation (e.g. babcess or an active arteriosclerotic lesion). Variant integrin containt integrin polypeptide integrin expression or activity, such as variant integrin polypeptide.
                                                           Disclosure; SEQ ID NO 7; 128pp; English.
as activation-dependent ligand.
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Sequence 198 AA;

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                                                                                                                                                                                                                                 61 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 120
                                                                                                                     CPTYMDVVIVLDGSNSIYPWSEVQTPLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 60
                                                                                             CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD
                                                                                                                                                                                                                                                                                                         121 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 176
                                                                                                                                                                                                                                                                                 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
                                                Gaps
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0
  Length 198;
Query Match 89.0%; Score 912; DB 8; Length 19
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 176; Conservative 0; Mismatches 0; Indels
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Human integrin alpha subunit Alpha 11 variant A domain.
        AAU76863 standard; protein; 193 AA
                         (first entry)
                          21-MAY-2002
                 AAU76863;
    RESULT
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Human, integrin alpha subunit, A domain, Alpha 11, integrin beta subunit, A-like domain, inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; mutant, antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy; mutein. Homo sapiens. Synthetic.

Misc-difference

/note= "Wild-type Ile substituted by any other amino Location/Qualifiers WO200209737-A1

Human, integrin alpha subunit, A domain, Alpha 11; integrin beta subunit, Alike domain; inflammatory disorder; skeletal muscle injury, restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.

Human integrin alpha subunit Alpha 11 A domain.

(first entry)

21-MAY-2002

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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin alpha subunit A domain. The polypeptide, preferably the collib alpha subunit A domain, where I at residue 320 have been replaced by CC GO A, F at residue 313 and A at residue 320 have been replaced by CC GO A, F at residue 313 and A at residue 320 have been replaced by CC GO A at residue 315 and A at residue 320 have been replaced by CC CO V at residue 315 and A at residue 320 have been replaced by CC CO V at residue 315 and A at residue 320 have been replaced by CC CO V at residue 315 and A at residue 320 have been replaced by CC CO V at residue 315 and A at residue 320 have been replaced by CC CO V at reating an inflammatory discreter, by contacting a test compound with the polypeptide and determining if the test compound binds CC to the polypeptide and determining if the test compound binds selected muscle injury, for treating disorders caused by ischaemia.

CC reperfusion injury, immune complexes, restencis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in CC two-hybrid our trace-hybrid assays. This sequence represents a human complexed integrin alpha subunit Alpha 11 variant A domain. Note: This variant sequence is not featured in the specification but has been derived from the wild-type protein shown in AAU76854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S| SPDLEKVIQQSERDNVTRYAVAVLGYYNRRGINPETFLNEIKYIASDPDDKHFFNV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU76854 standard; protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 57; Page; 55pp; English.
                                                                                                   31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                             31-JUL-2001; 2001WO-US023957
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nes 96; Conservative
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                                                                                                                                                                                                                                Li R,
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                   07-FEB-2002
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82 9 Location/Qualifiers

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                                                                                                                                                                                                                                                                                                      The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin better authority. The polypeptide, preferably the control alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CDIB or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemiar reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human thegrin alpha subunit Alpha 11 A domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YRSVKDVVBAASHIEQRGGTETRTARGIEFARSEAFQK--GGRKGAKKVMIVITDGESHD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
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                                                                                                                                                                                                                                Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.4e-48
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                                                                                                  31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                                          31-JUL-2001; 2001WO-US023957
                                                                                                                                                                              Arnaout AM, Li R, Xiong J;
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                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193 AA;
                         WO200209737-A1
 Homo sapiens.
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                                                 07-FEB-2002.
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The present sequence is that of the human integrin alpha 11 subunit A domain. This includes an invariant Ile residue. The invention features covariant integrin alpha subunit polypeptides in which the invariant Ile is substituted by Gly, Ala or some other amino acid (e.g. Val) or is caleted. The polypeptide can include part or all of the A domain. Comparing the invariant Ile creates a variant integrin polypeptide that is solution has a greater proportion of ligand. Forming polypeptides than the wild-type form of the subunit. Variant integrin polypeptides of the invention are useful in assays for compounds that bind to a variant ligand, that interfere with or enhance the binding of an integrin ligand to integrin, and for identifying activation. Some such antibodies, which bind to the high efficiency form of an integrin. Some such antibodies recognise an epitope that is either not present or not accessible on an integrin that is in a lower affinity conformation. The invention also provides methods of administering a variant integrin polypeptide, or an antibody that selectivity binds it, to identify a ligand which binds to an active integrin. Such assays are useful for diagnosing inflammation, e.g. occult inflammation (e.g. to identify a ligand which binds to an active integrin integrin con active and an active and antibody the selectivity binds it, con abscess or an active and exteriosclerotic leasion. Variant integrin polypeptide ligand and to treat disorders associated with a cherrant or unwanted integrin expression or activity, such as variant and antibod and to treat disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CQTYMDIVIVLDGSNSIYPWVEVQHFLINILKKFYIGFGQIQVGVVQYGEDVVHEFHLND 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, useful for
to CD11b, and for determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5%; Pred. No. 6.5e-48;
Matches 96; Conservative 31; Mismatches 47; Indels
                                                                                                                     /note= "Invariant Ile residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel variant integrin CD11b alpha subunit determining candidate compound for binding compound as activation-dependent ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 8; 128pp; English.
                                       /label = A_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2002; 2002US-00144259.
                                                                                                                                                                                                                                                                                                                                                                             12-MAY-2003; 2003WO-US014919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiong J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-593980/57
                                                                              Misc-difference 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENBANK; NP 036343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 196 AA;
                                                                                                                                                                                                            #O2004066914-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arnaout MA,
                                                                                                                                                                                                                                                                                               12-AUG-2004
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Domain
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82

142

ADR23225 RESULT

Homo sapiens

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Novel variant integrin CD11b alpha subunit polypeptide, useful for determining candidate compound for binding to CD11b, and for determining compound as activation-dependent ligand.
                                                         Human; integrin; CD49a; inflammation; antiinflammatory; vasotropic.
                                                                                                                    /note= "Invariant Ile residue"
                                          Human integrin CD49a alpha subunit A domain.
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5; 128pp; English.
                                                                                       Location/Qualifiers
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                                                                                              1. .195
/label = A_domain
ADR23225 standard; protein; 198
                                                                                                                                                               12-MAY-2003; 2003WO-US014919
                                                                                                                                                                               10-MAY-2002; 2002US-00144259
                                                                                                                                                                                                             Xiong J;
                            (first entry)
                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                           WPI; 2004-593980/57
                                                                                                             Misc-difference 193
                                                                                                                                                                                                             Li R,
                                                                                                                                                                                                                                   GENBANK; P56199.
                                                                                                                                  WO2004066914-A2
                                                                         Homo sapiens
                                                                                                                                                                                                             Arnaout MA,
                            04-NOV-2004
                                                                                                                                                 12-AUG-2004.
              ADR23225;
                                                                                              Domain
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domain. This includes an invariant limiter and the invention features variant integrin alpha subunit polypeptides in which the invariant Ile is substituted by Gly, Ala or some other amino acid (e.g. val) or is deleted. The polypeptide can include part or all of the A domain.

C deleted. The polypeptide can include part or all of the A domain.

C seplacing the invariant Ile creates a variant integrin polypeptide that its more active (i.e. in solution has a greater proportion of ligand-forming polypeptides of the invaniton are useful in assays for compounds that bind to a variant ligand, that inteffere with or enhance the binding of an integrin polypeptides of the invention are useful in assays for compounds that bind to a variant ligand, that inteffere with or enhance the binding of an integrin. Some such antibodies, which bind to the high efficiency form of an integrin. Some such antibodies recognise an epitope that is either not present or not accessible on an integrin that is in a lower affinity conformation. The invention also provides methods of administering a variant integrin polypeptide, or an antibody that selectivity binds it, to identify a ligand which binds to an active integrin. Such assays are useful for diagnosing inflammation, e.g. occult inflammation (e.g. abbress or an active antegrin. Such assays are abbress or an active antegrin integrin.
present sequence is that of the human integrin alpha subunit CD49a A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides can also be used to affect the bioavailability of a variant integrin polypeptide ligand and to treat disorders associated with aberrant or unwanted integrin expression or activity, such as vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 198 AA;
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                                                                 CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 82
                                                                                   Gaps
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41.7%; Score 427; DB 8; Length 198; 46.6%; Pred. No. 2.1e-40; ive 33; Mismatches 61; Indels
                 Local Similarity 46.6
1es 82; Conservative
                                                                 23
                                Matches
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Query Match

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Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atheroselerosis; thyroiditis; apissic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; fusion protein; rat.
FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The antibodies are useful for preventing or treating VLA-1 mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastrogastritesities integrinal conditions (e.g. inflammatory bowel disease, Crohn's disease, yastrogastritis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczemaburns, dermatitis, and abnormal proliferation of hair follicle cells or
                                                                            143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFRNV 198
                                                                                                 present invention relates to novel antibodies that
                                                                                                                                                                                                                                                                                                                                                                    Rat-human alpha 1-I domain fusion protein, RdeltaH.
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                                                                                                                                                                                                                        AAE33535 standard; protein; 192 AA
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06-JUL-2001; 2001US-0303689P.
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                         (revised)
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02-APR-2003
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83
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                                                  autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthitis, systemic lupus erythematosus and multiple sclerosis), renal fallure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft wersus host disease, conjunctivitis, swelling occurring after injury, myocardial ischaemia or endotoxin shock syndrome. The present sequence is rat-human alpha 1-I domain fusion protein, RdeltaH. This sequence is in the exemplification of the invention. (Updated on 23-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; escame; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthms; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn; disease; liritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anemais; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; praft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; alpha 1-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 TKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDGE 144
     periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 TYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQLDIVIVLDGSNSIXPWESVIAFLADLLKRMDIGPKQTQVGTVQYGENVTHEFNLNKYS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RLKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFNV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.4%; Score 424; DB 6; Length 192;
47.1%; Pred. No. 4.5e-40;
tive 33; Mismatches 59; Indels
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nes 82; Conservative
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Matches
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AAE33537
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Rat; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; ezcama burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; acthms; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anemais; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple solerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; alpha 1-1 protein.

Rattus

New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-

AAE33536 standard; protein; 192 AA

AAE33536

Rat alpha 1-I domain protein #1. 02-APR-2003 (first entry)

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The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disporders. The antibodies are useful for preventing or treating VLA-1: canditions (e.g. psoriatis, oczema, burns, dermatitia and abnormal conditions (e.g. psoriatis, cezema, burns, dermatitia and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, confitis, tendonitis, bursitis, fever, migrafune headches, gastrotine the achonitis, bursitis, fever, migrafune headches, gastrotine the achonitis, bursitis, fever, migrafune headches, gastrocintestrial irritable bowel syndrome, colitis and colorectal cancer), cascular diseases (e.g. atherosaclerosis), thyrodiditis, aplastic anaemia, contoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthritis, systemic lupus erythematosus and multiple sclerosis), renal fallure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, olymositis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft confirmediate hypersensitivity, graft and transplant rejections, graft confirmatial ischaemia or endotoxin shock syndrome. The present sequence is the minantic or minantic or endotoxin shock syndrome. The present of the the confirmation of the the semplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 TKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDGE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 TYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TQLDIVIVLDGSNSIYPWDSVTAFLNDLLKRMDIGFKQTQVGIVQYGENVTHEFNLNKYS 60
ed immunological or inflammatory disorders, e.g. psoriasis, eczem dermatitis, and abnormal proliferation of hair follicle cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RLKKVIQDCEDENIQRFSIAILGSYNRGNLSTEKFVEEIKSIASEPTEKHFFWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.4%; Score 424; DB 6; ilarity 47.1%; Pred. No. 4.5e-40; Conservative 33; Mismatches 59;
                                                                                                          Example 24; Page 94; 248pp; English.
  mediated immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention
                                                     fibrosis.
                              ourns,
  임
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Human integrin alpha subunit Alpha 1 (CD49a) A domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The antibodies are useful for preventing or treating VLA-1 antibodies are useful for preventing VLA-1 antibodies or inflammatory distress syndrome, asthma, proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, breakitis, freitable bowel syndrametory bowel disease, Crohn's disease, conscitution and antibodies, irritable bowel syndrame, colitis and colorectal cancer), vascular diseases (e.g. type I diabates, myasthenia gravis, rheumatoid autoimmune diseases (e.g. type I diabates, myasthenia gravis, rheumatoid arthitis, systemic lupus erythematosus and multiple sclerosis), renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft versus host disease, conjunctivitis, such shock syndrome. The present sequence is rat 1-I domain protein. This sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEEVLVAANKIGRQGGLQTMTALGIDTARKEAFTEARGARGVKKVWVIVTDGESHDNY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 TKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDGE 144
                                                                                                                                                                                                                                             anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
iated immunological or inflammatory disorders, e.g. psoriasis, eczema,
1s, dermatitis, and abnormal proliferation of hair follicle cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 TYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RLKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFRVV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.9%; Score 419; DB 6; Length 192;
46.6%; Pred. No. 1.7e-39;
iive 33; Mismatches 60; Indels
                                                                                                                                                                                    Karpusas M;
                                                                                                                                                                                                                                                                                                                          Example 24; Page 93-94; 248pp; English.
                                                                                                                                                                                   Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU76851 standard; protein; 195 AA
                                                                          12-APR-2002; 2002WO-US011521.
                                                                                                       13-APR-2001; 2001US-0283794P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 46.6
Les 81, Conservative
                                                                                                                                                                                   Lyne PD, Garber EA,
                                                                                                                                                                                                                WPI; 2003-093009/08.
                                                                                                                                                      (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 192 AA;
            WO200283854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-2002
                                           24-OCT-2002
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                                                                                                                                                                                                                                                             mediated
                                                                                                                                                                                                                                                                                           fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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ID AAU7
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AC AAU7
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142
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Human, integrin alpha subunit; A domain, CD49a; integrin beta subunit; A-1ike domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 1; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSTQLDIVIVLDGSNSIYPWDSVTAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.7%; Score 417; DB 5; Length 195; 45.5%; Pred. No. 3e-39; Artive 34; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 5; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU76860 standard; protein; 195
                                                                                                                                                                                                                                           31-JUL-2000; 2000US-0221950P.
                                                                                                                                                                                                        31-JUL-2001; 2001WO-US023957
                                                                                                                                                                                                                                                          11-JAN-2001; 2001US-00758493
13-MAR-2001; 2001US-00805354
                                                                                                                                                                                                                                                                                                                                                       Xiong J;
                                                                                                                                                                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-188687/24.
                                                                                                                                                                                                                                                                                                                                                       Li R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 195 AA;
                                                                                                                               WO200209737-A1
                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mac
Local Sim
80;
                                                                                                                                                                   07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                       Arnaout AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU76860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Thu Apr

121 NHRLKKVIQDCEDENLQRFSIAILGSYNRGNLSTEKFVEELKSIASEPTEKHFFNV 176

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Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit; A-like domain; inflammatory disorder; skeletal muscle injury; restenosis; 1schaemia-reperfusion injury; immune complex; parasitic disease; mutant; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                         Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                                                                               /note= "Wild-type Ile substituted by any other amino
           Human integrin alpha subunit Alpha 1 (CD49a) variant A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived from the wild-type protein shown in AAU76851
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                      31-JUL-2000; 2000US-0221950P.
11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 45; Page; 55pp; English
                                                                                                                                                                                                                                                31-JUL-2001; 2001WO-US023957.
                                                                                                                                                                                                                                                                                                                                          Li R, Xiong J;
                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-188687/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 195 AA;
                                                                                mutein; Alpha 1
                                                                                                                                                     Misc-difference
                                                                                                                                                                                                    WO200209737-A1
                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                              Arnaout AM,
                                                                                                                                                                                                                          07-FEB-2002
                                                                                                                   Synthetic.
                                                                                                        Homo
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the coll b alpha subunit A domain, where I at residue 312 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or C or determining if a test compound is a candidate compound for binding to coll b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing selectal muscle injury, immune complexes, restences caused by ischemianing two-hybrid or three-hybrid assays. This sequence represents a human two-hybrid or three-hybrid assays. This sequence represents a human contact in the contact in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSTOLDIVIVLDGSNSIYPWDSVTAFLNDLLKRMDIGPKOTOVGIVOYGENVTHEFNLNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence is not featured in the specification but has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.7%; Score 417; DB 5 45.5%; Pred. No. 3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFRNV 198

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The present sequence is that of the human integrin alpha subunit CD49b A domain. This includes an invariant Ile residue. The invention features variant integrin alpha subunit polypeptides in which the invariant Ile is substituted by Gly, Ala or some other amino acid (e.g. Val) or is deleted. The polypeptide can include part or all of the A domain. Replacing the invariant Ile creates a variant integrin polypeptide that is solution has a greater proportion of Ilgand. Replacing polypeptides of the invention are useful in assays for compounds integrin polypeptides of the invention are useful in assays for compounds that bind to a variant ligand, that intefre with or enhance the binding of an integrin ligand to integrin, and for identifying activation. Specific Ilgands. They are also useful for generating antibodies, e.g. monoclonal antibodies which bind to the high efficiency form of an integrin shows matibodies recognise an epitope that is either not present or not accessible on an integrin that is in a lower affinity conformation. The invention also provides methods of administering a variant integrin polypeptide, or an antibody that selectivity binds it, to identify a ligand which binds to an active integrin. Such assays are useful for diagnosing inflammation, e.g. occult inflammation (e.g. abscess or an active integrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides can also be used to affect the bioavailability of a variant integrin polypeptide ligand and to treat disorders associated with aberrant or unwanted integrin expression or activity, such as vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide, useful for
to CD11b, and for determining
                                                                                                                                                                                       Human; integrin; CD49b; inflammation; antiinflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 399; DB 8; Length 198; Pred. No. 3.6e-37;
                                                                                                                                                                                                                                                                                                                                         /note= "Invariant Ile residue"
                                                                                                                                                  Human integrin CD49b alpha subunit A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel variant integrin CD11b alpha subunit determining candidate compound for binding compound as activation-dependent ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 6; 128pp; English
                                                                                                                                                                                                                                                               Location/Qualifiers
                                       Ź
                                                                                                                                                                                                                                                                                 1. .195
/label = A_domain
                                     ADR23226 standard; protein; 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-2003; 2003WO-US014919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2002; 2002US-00144259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiong J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP.
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-593980/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENBANK; NP 002194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                              WO2004066914-A2
                                                                                                                                                                                                                            Homo sapiens
                                                                                                               04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnaout MA,
                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
                                                                          ADR23226;
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                                                                                                                                                                                                                                                                                     Domain
RESULT 13
                   ADR23226
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142

FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD

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                                                                                                                  FRIKEEVVRAAKNISRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLIVVVTDGESHD 142
                                                    agent that prevents or treating human or non-
                               CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD
                                                                                                                                                                                 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
     Gaps
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Best Local Similarity 46.0%; Pred. No. 1.8e-36;
Matches 81; Conservative 28; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Anthrax; toxin; receptor; integrin; human; antibacterial.
   66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mogridge JS;
 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31-32; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collier RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human animal suffering from anthrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                            ABP54908 standard, protein, 198 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2001; 2001WO-US030941
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Integrin alpha-2 I domain.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young JAT, Bradley KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-713235/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                          08-JAN-2003
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81;
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                                                                                                                                                                                                                                                                                                          ABP54908;
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 Matches
                                                                                                                                                                                                                                              RESULT 14
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ID ABP5
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The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, or Or A, T at the compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by isohaemia-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                    Human, integrin alpha subunit, A domain, CD49b; integrin beta subunit; A Like domain; inflammatory disorder; skeletal muscle injury; restenosis; sichaemia-reperfusion injury; immune complex; parasitic disease; Alpha 2; antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
                                                                                                                                                                               GSMLKAVIDQCNHDNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNV 176
                                                                                                                                       143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human integrin alpha subunit Alpha 2 (CD49b) A domain.
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                                                                                                                                                                                                                                                                                                                                                                                    AAU76852 standard; protein; 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2001; 2001US-00758493.
13-MAR-2001; 2001US-00805354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Simi
Matches 79;
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CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 82 CPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGFTKTQVGLIQYANNFRVVFNLNT 60

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1 CPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNT 60
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Search completed: April 6, 2005, 14:36:34 Job time : 180 secs

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1 GICARVDASFQPQGSLAPTA......FLREIRTIASDPDERFFFNV 198
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-647-544-2_COPY_140_337
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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* Query	Match	89.0	89.0	89.0	48.0	48.0	48.0	41.7	41.7	41.7	41.4	41.4	40.9	40.9
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US-09-805-354-6 Sequence 6, Appli US-09-764-893-6 Sequence 6, Appli US-10-144-259-6 Sequence 6, Appli US-10-144-259-6 Sequence 284, Appli US-10-125-540-284 Sequence 284, Appli US-10-125-540-284 Sequence 444, Appli US-09-764-870-472 Sequence 472, Appli US-09-764-875-1193 Sequence 472, Appli US-09-976-782-38 Sequence 38, Appli US-10-10-15-540-472 Sequence 313, Appli US-10-346-863-31 Sequence 31, Appli US-10-346-863-31 Sequence 31, Appli US-10-346-863-30 Sequence 31, Appli US-10-346-863-40 Sequence 31, Appli US-10-004-378A-81 Sequence 31, Appli US-10-004-378A-81 Sequence 31, Appli US-10-144-259-3 Sequence 31, Appli US-10-346-863-33, App	Sequence 35, Sequence 36, Sequence 41, Sequence 41, Sequence 41,	15354 11TY INTEGRIN POLYPEPTIDES AND USES THEREOF 1/09/805,354 04 19/758,493 10/221,950 Version 4.0	89.0%; Score 912; DB 10; Length 195; imilarity 100.0%; Pred. No. 2.1e-89; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CPTYMDVVIVLDGSNSIXPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 82
1000 100 100 100 100 100 100 100 100 10	883 883 11 84 11 11	on US/09805 330078375A1 M. Amin 1:an-Ping HIGH AFFINI (6-53601) NUMBER: US 09 MBER: US 09 MBER: US 09 000-07-31 i: 20 or Windows V	\$0 ISI
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399 399 3999 2885.59 2885.59 2885.71 1170 1170 1170 1170 1170 1170 1170 1	44 L L L L L L L L L L L L L L L L L L	ESULT 1 S-09-805-354-7 Sequence 7, Applic Sequence 7, Applic APPLICATI Arnaou APPLICANT: Arnaou APPLICANT: Ainaou APPLICANT: Ainaou TITLE OF INVENTIO PRIOR FILING DATE TOWNBER OF SEQ ID SOFTWARE: FASTSEQ SEQ ID NO 7 LENGTH: 195 TYPE: PRI ORGANISM: HOMO 8 IS-09-805-354-7	(atch)cal 3 17 23
	O H W A A A	RESULT 1 US-09-805- Sequence Publicate APPLICP APPLICP APPLICP TITLE C TITLE C TITLE C TITLE C PRIOR P PRIOR P PRIOR P PRIOR P PRIOR P PRIOR P SEQ ID N SOFTWARN SOFT	Query N Best Lo Matcher Qy Db

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FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 120
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                                                                                                  FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGPSQSHGGRPEAARLLVVVTDGESHD 142
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                                          1 CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTYON: HIGH APPINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00786-536001
CURRENT APPLICATION NUMBER: US/09/805,354
CURRENT FILING DATE: 2002-06-04
PRIOR PILING DATE: 2001-01-11
PRIOR PLING DATE: 2001-01-11
PRIOR PLING DATE: 2001-01-3
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 193
CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD
                                                                                                                                                                                                       143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
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US-09-758-493-8

i Sequence 8, Application US/09758493

j Publication No. US20040086935A1

j Publication No. US20040086935A1

j GENERAL INFORMATION:
    APPLICANT: Arnaout, M. Amin

j APPLICANT: Aing, Jian-Ping

TITLE OF INVENTION: HIGH APPINITY INTEGRIN POLYPEPTIDES AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 0078-6-8044001

CURRENT APPLICATION NUMBER: US/09/758,493

CURRENT APPLICATION NUMBER: US 60/221,950

PRIOR FILING DATE: 2000-07-31

j RNDHER OF SEQ ID NOS: 20

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09805354
Publication No. US20030078375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Arnaout, M. Amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-805-354-8
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                          143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
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143 GEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
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APPLICANT: Li, Rui

APPLICANT: Li, Rui

APPLICANT: Li, Rui

APPLICANT: Along, Jian-Ping

TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF

FILE REPERRICE: 00786-548001

CURRENT APPLICATION NUMBER: US/10/144,259

CURRENT FILING DATE: 2000-004

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 7
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: 00786-804001
CURRENT APPLICATION NUMBER: US/09/758,493
CURRENT FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 20
SOFFWARE: PastSEQ for Windows Version 4.0
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89.0%; Score 912; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels (
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89.0%; Score 912; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels
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// Publication No. US20030109691A1
// GENERAL INFORMATION:
                                                                                                                                                                       Sequence 7, Application US/09758493
Publication No. US20040086935A1
GENERAL INFORMATION:
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US-10-144-259-7
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ORGANISM: Homo sapiens
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LENGIH: 195
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APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Nois, Jian-Ping
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REPERENCE: 00786-536001
CURRENT APPLICATION NUMBER: US/09/805,354
                                                                                                                                     23 CPTYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGD
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                                                        ch 48.0%; Score 492; DB 11; Length 193; Similarity 54.5%; Pred. No. 2.5e-44; 96; Conservative 31; Mismatches 47; Indels
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Publication No. US20030109691A1
GENERAL INFORMATION:
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US-10-144-259-8
; ORGANISM: Homo sapiens
US-09-758-493-8
                                                                          Best Local Similarity
Matches 96; Conserv
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US-09-805-354-5
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83 FRIKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSOSHGGRPEAARLLVVVTDGESHD 142
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Sequence 5, Application US/09758493;
Publication No. US20040086935A1;
Publication No. US20040086935A1;
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
APPLICANT: Arnaout, M. HIGH ARPLINITY INTEGRIN POLYPEPTIDES AND TITLE OF INVENTION: USES THEREOF;
FILE REPRENENCE: 00786-804001;
CURRENT APPLICATION NUMBER: US/09/758,493;
CURRENT FILING DATE: 2001-01-11;
PRIOR FILING DATE: 2000-07-31;
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                 Length 195;
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41.7%; Score 427; DB 11;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61;
                                                                                                                                                                                                                                                                                                          Query Match
41.7%; Score 427; DB 10;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61;
CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US 09/758,493

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 195
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US-10-144-259-5
; Sequence 5, Application US/10144259
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US-09-758-493-5
                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-805-354-5
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61 STEEVLVAANKIVQRGGRQTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNY 120
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                                                                                 145 ELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSPLREIRTIASDPDERFFRV 198
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                                                                                                                             121 RLKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFFNV 174
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APPLICANT: PRELPS, CHRISTOPHER BENJAMIN
APPLICANT: PAGAN, RICHARD JOSEPH
APPLICANT: GUTTERINGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT APPLICATION NUMBER: PCT/GB01/03318
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATCHIL OF SEQ ID NOS: 57
LENGTH: 192
TYPE: PRI
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Publication No. US20040038325A1
GENERAL INFORMATION:
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Best Local Similarity 47.1%;
Matches 82; Conservative
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; ORGANISM: Homo sapiens
US-10-474-832-61
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US-10-346-863-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 GEBLPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLRBIRTIASDPDERFFFNV 198
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Atmock, M. Amin
APPLICANT: Atmock, Jan-Ping
ITILE OF INVENTION: UMRIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REPRENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
PRIOR APPLICATION NUMBER: US 09/758,493
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 5
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TITLE OF INVENTION: ANTIBODIES TO VLA-1
FILE REPERENCE: Alo1 PCT
CURRENT APPLICATION NUMBER: 06/283,794
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 59
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Publication No. US20040081651A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 82; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 00786-53601
CURRENT FILING DATE: 2002-06-04
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTERO FOR Windows Version 4.0
                                                                                                                   25 TYMDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDFR
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Best Local Similarity 46.6%; Pred. No. 1.7e-36;
Matches 81; Conservative 33; Mismatches 60; Indels
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JUNEAU AINCENTING.
JULIE OF INVENTION: ANTIBODIES TO VLA-1
FILE REFERENCE: ALOI PCT
CURRENT APPLICATION NUMBER: US/10/474,832
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/283,794
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-06
NUMBER: OF SEQ ID NOS: 70
SEQ ID NO 60
LENGTH: 192
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US-10-474-832-60
; Sequence 60, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION
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Publication No. US20030078375A1
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; ORGANISM: Rattus sp.
US-10-474-832-60
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Publication No. US20040086935A1

GRUERAL INFORMATION:

APPLICANT: Li, Rui

APPLICANT: Li, Rui

APPLICANT: Li, Rui

APPLICANT: Li, Rui

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REPRENCE: 00786-804001

CURRENT PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR APPLICATION NUMBER: US 60/221,950

NUMBER OF SEQ ID NOS: 20

NUMBER OF SEQ ID NOS: 20

SOPTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                Length 195;
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38.9%; Score 399; DB 11;
Best Local Similarity 46.0%; Pred. No. 2.5e-34;
Matches 81; Conservative 29; Mismatches 66;
                                                                                                                                                             Query Match
38.9%; Score 399; DB 10;
Best Local Similarity 46.0%; Pred. No. 2.5e-34;
Matches 81; Conservative 29; Mismatches 66;
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; SEQ ID NO 6
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-6
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US-09-758-493-6
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10334, A
10761, A
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Sequence 7, Appli
Sequence 7, Appli
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36123, A
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                                                                             6, 2005, 14:29:18; Search time 43 Seconds (without alignments) 343.733 Million cell updates/sec
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                                                                                                                                                    1 GICARVDASFQPQGSLAPTA.....FLREIRTIASDPDERFFFNV 198
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Sequence 61
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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-09-252-991A-21325
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US-08-974-899-8
US-09-795-798-8
US-08-6177-109A-61
US-08-65-178-61
US-09-513-999C-6277
US-09-252-991A-2132
US-09-252-991A-2975
US-09-902-540-10761
US-09-902-540-10761
US-08-462-128-38
US-09-902-540-10761
US-08-463-180-38
US-09-902-540-10761
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US-09-902-540-10761
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US-08-687-706-62
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1025
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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GENERAL INFORMATION:
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                                   64 XWXDPDALLXHVKHWLLL----TNTFGAINYVATEVFREELGARPDATXVLIIITDGEAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KRKDPDALLKHVKHMLLL----TNTFGAINYVATEVFREELGARPDATKVLIIITDGEAT 117
               84 -- RTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 --RTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 141
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                                                                               142 DGEELPAALKACEAGRVTRYGIAVLGHYLRRORDPSSFLREIRTIASDPDERF 194
                                                                                                                 120 DSGNIDAAKD-----IIRYIIGIGKHPQTKESQET----LHKFASKPASEF 161
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25.4%; Pred. No. 3.1e-10;
tive 37; Mismatches 70; Indels
                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINDatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 11/27/96

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1014R1

TELECOMPUNICATION INFORMATION:

TELEFAX: 650/255-1994

TELEFAX: 650/952-9881

INPORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids
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Best Local Similarity
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US-09-795-798-7
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62 KRKDPDALLKHVKHMILL----TNTFGAINYVATEVFREELGARPDATKVLIIITDGEAT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 MDVVIVLDGSNSIYP--WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDF-
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Fatent No. 5869615
GENERAL INFORMATION:
APPLICANT Dennis E. Hourcade and Teresa J. Oglesby TITLE OF INTENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patera L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
CONNTRY: USA
                      Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSES: Geneentech, Inc.
STRET: 1 DNA WAY
CITY: South, San, Prancisco
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: S8-Peb-2001
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.4%; Score 148; DB 4; ilarity 25.4%; Pred. No. 3.1e-10; Conservative 37; Mismatches 70.
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 184 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                         STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 44; Conserva
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PCT-US96-01314-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.3%; Score 147; DB 2; Length 187;
Best Local Similarity 26.7%; Pred. No. 4.2e-10;
Matches 48; Conservative 36; Mismatches 84; Indels 12; Gaps
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
PILING DATE: 03-JAN.1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION FORE OF 100: 62: SEQUENCE CHARACTERISTICS:
LEMETAL: 1404) 873-8795
INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS:
LEMETH: 13 mainto acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: LIGHTON MEST FEACHLIFE STITES
STATE: Georgia
COUNTRY: 30309-3450
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: 18P PLICATION NUMBER: US/08/687,706
FILING DATE: 26-JUL-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION: 514
ATTONEX/AGENT: NPORMATION:
NAME: PEDSE, PATENT INFORMATION:
NAME: PEDSE NAME: PATENT INFORMATION:
NAME: PATENT I
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Patent No. 5928892
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-177-109A-62
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140 SH-DGEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 LGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CPTY-MDVVIVLDGSNSIYP--WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.7%; Pred. No. 4.2e-10;
Matches 48; Conservative 36; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTR: U.S.A.

ZITE: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
APPLICATION UNBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELECOMMUNICATION INPORMATION:
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-687-706-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                  linear
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62 KQKDPDALLEHVKHMLLL----TNTFGAINYVATEVPREELGARPDATKVLIIITDGEAT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPBAARLLVVVTDGESH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VDLIFLFDGSMSLQPDEFQXILDFMXDVMKKL--SNTSYQFAAVQFSTSYKTEFDFSDYV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 MDVVIVLDGSNSIYP--WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | : | | | | DSGNIDAAKD-----IRYFASKPASEF 159
    118 DSGNIDAAKD-----IIRYIIGIGKHFQTKESQET-----LHKFASKPASEF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 DGEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71; Indels
                                                                                                                                                                                                                 Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       ADDRESSEE Genericch, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28 Feb-2001
CLASSIFICATION SATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application US/08177109A
Patent No. 5869615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 145; DB 4; ilarity 24.9%; Pred. No. 7.4e-10; Conservative 37; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P1014R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         APPLICANT: Presta, Leonard G.
                                                                                                                     ; Sequence 8, Application US/09795798; Patent No. 6703018; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 184 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 43; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-177-109A-61
                                                                                            US-09-795-798-8
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                                                                                                                                                                                                                                                                                                                   118 KEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNR-----NSWKELNDIASKPSQEHIFKV 172
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                                                                                                                                                                                      80 LGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGE 139
                                                                                                                                                                                                                                                                                   140 SH-DGEELPAALKACEAGRVTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDERFFFNV 198
                                                                                          23 CPTY-MDVVIVLDGSNSIYP--WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWS 79
                                                                                                                       27 MDVVIVLDGSNSIYP -- WSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSLGDF - 83
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                                                   12;
14.3%; Score 147; DB 5; Length 187; 26.7%; Pred. No. 4.2e-10; ive 36; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardiau, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Score 145; DB 3; 24.9%; Pred. No. 7.4e-10; ive 37; Mismatches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/974,899
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILLING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PIC
TELECOMMUNICATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 amino acids
                                              48, Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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: USA
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Best Local Similarity
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                   Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-974-899-8
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 VHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 VTDGESHDGEELPAALKACEAGR -- VTRYGIAVLGHYLRRQRDPSSFLREIRTIASDPDE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CPTY-MDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDP--EQIQ-----VGLVQYGESP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CPQEDSDIAFLIDGSGSIIPHD----FRRM--KEFVSTVMEQLKKSKTLFSLMQYSEEF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.0%; Score 144; DB 2; Length 187; Best Local Similarity 31.7%; Pred. No. 1e-09; Matches 59; Conservative 26; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, v
                                                                                                            ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION INBER: WU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5928892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : protein
NO
                                           CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 RFFFNV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-177-109A-61
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US-08-463-682-1

Sequence 1, Application US/08463682

Patent No. 6008193

GENERAL INFORMATION:

APPLICANT: Leonard Garfinkel, et al.

TITLE OF INVENTION: Willebrand Factor GPIb Binding Domain Polypeptides and TITLE OF INVENTION: Welhods of Using Same

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CPTY-MDVVIVLDGSNSIYPWSEVQTFLRRLVGKLFIDP--EQIQ-----VGLVQYGESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 VHEWSLGDFRIKEEVVRAAKNLSRREGREIKTAQAIMVACTEGFSQSHGGRPEAARLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

14.0%; Score 144; DB 2; Length 187;
Best Local Similarity 31.7%; Pred. No. 1e-09;
Matches 59; Conservative 26; Mismatches 77; Indels
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                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 03-0AN-1994
CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: PABSE, PATECA L.
REGISTRATION NUMBER: 31,284
REFERENCE, POCKET NUMBER: 31,284
REFERENCE, POCKET NUMBER: 40,107 DIV
TELECHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
                         US/08/687,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of Americas CITY: New York STATE: New York COUNTRY: U.S.A.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                  FILING DATE: 26
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 -------MASQEPQRMSRNFVRYV-QGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 HDGEELPAALKACEAGRVTRYGIAVLGHYLRRQR------DPSSFLREIRTIASD-PD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.,
APPLICANT: Duclert, A.,
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 673961
Patent No. 673961
PILE REPERBURE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1090-02-24
PRIOR PLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Petent.pm
SOFTWARE: Petent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                       23 CPTYMDVVIVLDGSN--SIYPWSEVQTFLRRLVGKLFIDPEQIQVGLVQYGESPVHEWSL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                      9.1%; Score 93; DB 3; Length 187; larity 20.7%; Pred. No. 0.0029; Conservative 46; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.1%; Score 73; DB 4; Length 77;
Best Local Similarity 40.0%; Pred. No. 0.25;
Matches 16; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2-Y
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acids
STRANDENESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6277, Application US/09513999C
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa=Cys or Gly US-09-513-999C-6277
                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 38; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 ERFF 195
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US-08-463-682-1
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US-09-513-999C-6277
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Sequence 21325, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-1136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
PRIOR PLING DATE: 1998-07-27
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10448-018001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 -----GEELPAALKA-----CEAGRVTRYGIAVLGHYLRRQRDPS----SFLREI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VMANNEQKRDEGYIEKLVQVNRVAKT-----VKGGRIFAFTALTVVGDGKGRVGFGRGKA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 LVRVAPSLFLGSARAAGAEEQLARAGVTLCVNVSRQQPGPRAPGVABLRVPVFDDPAEDL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 VVRAAKNL----SRREGRETKTAQAIMVACTEGFSQSHGGR-PEAARLLVVVTDGESHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 69; DB 4; Length 167; 38.7%; Pred. No. 2.7; tive 3; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.7%; Score 69; DB 4; Length 176; Best Local Similarity 28.0%; Pred. No. 2.9; Matches 37; Conservative 17; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kapeller, Rosanna
TITLE OF INVENTION:
1048-01801
CURRENT APPLICATION NUMBER: US/09/704,139
CURRENT APPLICATION NUMBER: US 60/185,772
PRIOR APPLICATION NUMBER: US 60/185,772
PRIOR PILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1). (1390)
OTHER INFORMATION: n = a, t, g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09704139 Patent No. 6420153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn version 3.0
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56 REVPAAIQKAMEAAR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.74
Matches 29, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin v
S-09-252-991A-21325
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LENGTH: 176
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137 RPVA-EPNPGFW 147

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Sequence 29795, Application US/09252991A

Sequence 29795, Application US/09252991A

Patent No. 6551795

GENERAL INCORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SPLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29795

LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 LVQYGESPVHEWSLGDFRT------KEEVVRAAKNLSRRE------GRETKT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AQAIMVACTEG----FSQSHGGRPEAARLLVVVTDGESHD---GEELPAALKACEAGRVT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 LPROGARPTPRGPLGGTPTIQPDTALLEQQGVLKKATARCAVQAGRGRGAAGPAGAPDRG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.7%; Score 68.5; DB 4; Length 177; Best Local Similarity 24.0%; Pred. No. 3.4; Matches 37; Conservative 14; Mismatches 62; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 RYGIAVLGHYLRRORDPSSFLREIRTIASDPDER 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 -----LAHQLRRRRAPALRVALLRQRQQPDHR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29795
RESULT 15
US-09-252-991A-29795
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Search completed: April 6, 2005, 14:41:28 Job time : 49 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

April Run on:

6, 2005, 13:33:34 ; Search time 42 Seconds '(without alignments) 80.181 Million cell updates/sec

1 YEVHPYGTLPVGPGPEFKTTLRVQNLGCYVVSGLI 35 US-09-647-544-2_COPY_952_986 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

7756 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* *:6/ PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	V3 domain peptide	steryl-sulfatase (dihydrolipoamide d	neurophysin 1 - ch	deoxynucleoside ki	hypothetical prote	V3 domain peptide	sperm-activating p	gene aeg-46.5 prot	T-cell receptor be	proline-rich antib	V3 domain peptide	29K antigen PEB2 -	hypothetical prote	걲	granulocyte inhibi	protein phosphatas	Ig kappa chain V-I	deoxycytidine kina	proteinase inhibit	hemopexin - chicke	V3 domain peptide	(S)-6-hydroxynicot	T-cell receptor al	hemagglutinin - In	T-cell receptor al	deoxynucleoside ki	ubiquinol-cytochro	fibronectin - mous
SUMMARIES	QI	PC2297	S05414	S13863	D61563	A54257	B36912	PC2295	H60588	I69492	PQ0070	S74112	PC2296	B41161	AD2525	S68394	A36016	T42441	B30609	A31859	JN0366	C31514	PC2294	S18264	C32537	PL0161	D32537	C54257	S41774	148349
	DB	7	~	~	7	~	~	~	7	7	~	~	~	0	~	N	N	~	~	~	~	~	~	0	~	~	7	~	~	7
	Query Match Length	35	26	33	33	35	35	35	10	30	22	30	35	35	35	19	20	24	24	28	28	34	35	35	18	20	22	27	28	28
	Query Match	9.3	8.8	8.5	•	8.2	8.0	7.7	7.2	7.2	6.7	6.7	6.7	6.7	6.4	6.1	6.1	6.1	6.1	6.1	6.1		5.9	٠	٠	9.9	9.6	9.6		
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	Score	37	36	35.5	35	35	34.5	34		33	32	32	32	32	31.5	31		31		31	31	m	30.5				30	30		
	Result No.	1	7	m	4	Ŋ	9	7	89	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 3 S13863

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hypothetical prote hypothetical prote V3 domain peptide	aldose 1-epimerase cytochrome P450K-2 LX-1 tumor antigen formin hinding nor	transforming prote V3 domain pepiide pepsin I (EC 3.4.2 Neb-colloostatin -	immunodeficiency v aldose l-epimerase Ig kappa chain V-I Ig heavy chain V r Ig kappa chain V-I
A95047 H95019 PC2293	A24487 S08282 A39269	234874 PC2298 A60507 S69153	S65399 PU0033 B130608 S36378 G30608
0 0 0	0000	0000	00000
33 34 5	27 22 22	30 33 13	20 22 28 28 29
15.6 15.6 15.6	15.4	15.1 15.1 14.8	14.6 14.6 14.6 14.6
30	29.5 29 29	28.59 28.59 28.59	0 0 0 0 0 0
30 31		7 8 8 8 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 1 2 8 4 3

ALIGNMENTS

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PC2297
V3 domain peptide P4611 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: PC2297
C;Accession: PC2297
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a. A;Reference number: PC2291; MUID:95110306; PMID:7811250
A;Accession: PC2291
A;Accession: PC2291
A;Residues: 1-35 cSHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stery1-sulfatase (BC 3.1.6.2), microsomal - rat (fragment)
NyAlternate names: arylsulfatase C
C;Species: Rattue norvegicus (Norway rat)
C;Species: Rattue norvegicus (Norway rat)
C;Accession: 505414
S;Kawano, J.I.; Kotani, T.; Ohtaki, S.; Minamino, N.; Matsuo, H.; Oinuma, T.; Aikawa, E.
Biochim: Biophys: Acta 997, 199-205, 1989
A;Title: Characterization of rat and human steroid sulfatases.
A;Reference number: S05414; MUID:89352671; PMID:2765556
A;Accession: S05414
A;Molecule type: protein
A;Residues: 1-26 <KAM>
C;Keywords: sulfuric ester hydrolase
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C;Superfamily: type B retrovirus env polyprotein
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Best Local Similarity 40.9<sup>3</sup>
Matches 9; Conservative
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11 SIPIGPGRALYTT 23
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A; Accession: H60588
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deoxynucleoside kinase complex I S-component - Lactobacillus acidophilus (fragment)
C/Species: Lactobacillus acidophilus
C/Species: Lactobacillus acidophilus
C/Date: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A54257
C/Accession: A54257
Biochemistry 33, 5328-5334, 1994
A/Title: Heterodimeric deoxynucleoside kinases of Lactobacillus acidophilus R-26: functi
A/Reference number: A54257
A/Accession: A54
dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Trypanosoma cruzi (fragment)
Cjspecies Trypanosoma cruzi
Cjspecies Trypanosoma cruzi
Cjacesion: 813863
Klohrer, H.; Krauth-Siegel, K.L.
Eur. J. Blochem. 194, 863-869, 1997
A,Title: Purification and characterization of lipoamide dehydrogenase from Trypanosoma A,Reference number: 813863; MUID:91099369; PMID:2269305
A,Accession: 813863
A,Residunis Lype: protein
A,Residunis Lype: protein
A,Residunis Lype: protein
Cjsuperfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology Cjsuperfamily: dihydrolipoamide dehydrogenase homology Cjsuperfamily: dihydrolipoamide beta FAD nucleotide-binding fold
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Chicken
Cipace: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
Cipace: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
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18.5%; Score 35.5; DB 2; Length 33;
Best Local Similarity 31.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 3; Mismatches 6; Indels
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A,Experimental source: R-26
A,Note: sequence extracted from NCBI backbone (NCBIP:146748)
C,Superfamily: Lactobacillus acidophilus deoxyadenosine kinase
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C; Superfamily: oxytocin-neurophysin
C; Keywords: hormone
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C;Species: Eubacterium sp.
C;Date: 07-Apr.1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: B35912
R;Franklund, C.V.; Baron, S.F.; Hylemon, P.B.
J. Bacteriol. 175, 3002-3012, 1993
A;Title: Characterization of the baiH gene encoding a bile acid-inducible NADH:flavin ox. A;Reference number: A36912; MUID:93259945; PMID:8491719
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C;Superfamily: type E retrovirus env polyprotein
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C;Species: Heterocentrotus
C;Species: Heter
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R; Sherefa, K.; Scennerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping A;Reference number: PC2291; MUID:95110306; PMID:7811250
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C;Date: 21-Feb_1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
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10 PVGPGPEFKTTLRVQNLG 27
                                                                                                                 7 PIGAGKSSLTSLLAEXLG 24
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11 SIHIGPGRAFYTT 23
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C,Accession: PC2296
R,Sherefa, K.; Scennerborg, A.; Steinbergs, J.; Saellberg, M.
R,Sherefa, K.; Scennerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A,Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a. A;Reference number: PC2291; MUID:95110306; PMID:7811250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein asr7380 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al C; Species: Nostoc sp. PCC 7120 Ashote: Nostoc sp. PCC 7120 (sp. strain PCC 7120) as synonym of Anabaena sp. strain PCC 7120 (c; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C; Accession: AD2525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: B41161
R;Pei, Z.; Ellison III, R.T.; Blaser, M.J.
N. Biol. Chem. 266, 16363-16369, 1991
A;Title: Identification, purfication, and characterization of major antigenic proteins A;Reference number: A41161; MUID:91358413; PMID:1885571
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C;Species: Campylobacter jejuni
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                               V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8e+02;
                                                                                                                                     Query Match 16.7%; Score 32; DB 2; 1 Best Local Similarity 45.5%; Pred. No. 7.4e+02; Matches 5; Conservative 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.7%; Score 32; DB 2; 47.1%; Pred. No. 8.8e+02
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C;Superfamily: type E retrovirus env polyprotein
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                    A, Cross-references: UNIPROT: P82964
A, Experimental source: haemocytes
C, Keywords: antibacterial
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Matches 8; Conservative
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                   5 PYGTLPVGPGP 15
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8 PFPRPPIGPRP 18
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A;Molecule type: protein
A;Residues: 1-35 <PEI>
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A; Residues: 1-30 <SCH>
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C;Species: Carcinus maenas (green crab, common shore crab)
C;Date: ll-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S74112
R;Schapp, D.; Kemp, G.D.; Smith, V.J.
Eur. J. Biochem. 240, 532-539, 1996
A;Title: Purification and characterization of a proline-rich antibacterial peptide, with A;Reference number: S74112; MUID:97008941; PMID:8856051
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: 169492
R;Choe, M.; Reznikoff, W.S.
Bacteriol. 175, 1165-1172, 1993
A;Title: 1dentification of the regulatory sequence of anaerobically expressed locus aeg-A;Reference number: 154984; MUID:93163046; PMID:8432709
A;Accession: 169492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q53301; GB:S54754; NID:g265388; PIDN:AAB25330.1; PID:g265389
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Bacte: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C;Accession: PQ0070
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.
S;Danitted to JIPID, May 1990
A;Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A;Reference number: JQ0472
A;Accession: PQ0070
                                                                                                                                                                                                                                                                                                                                    C.Species: Escherichia coli
C.Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
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Pred. No. 5.3e+02;
0; Mismatches 3; Indels
     Length 10;
17.2%; Score 33; DB 2; 175.0%; Pred. No. 1.6e+02; ive 0; Mismatches 2
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1 MHPVGAYSLVAGAKPVTVSVRPGP-----VMNL 28
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A;Molecule type: DNA
A;Residues: 1-30 <RES>
                                                                                                                                                                                                                                                                                                          protein - Escherichia coli
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Matches 6; Conservative
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A; Residues: 1-22 <TAN>
A; Experimental source: T cell
C; Genetics:
                                                         Conservative
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                                                                                                              GTLPVGPG 14
                                                                                                                                                                  GTLPTGSG 8
Query Match
Best Local Similarity
Matches 6; Conserv
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C,Keywords: receptor
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REBULT 15
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H-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii (fra
N.Alternate names: ATP synthase chain G
C/Species: Chlamydomonas reinhardtii
C/Species: Chlamydomonas reinhardtii
C/Accession: S68397
Requence_revision 12-Dec-1997 #text_change 09-Jul-2004
C/Accession: S68394
R.Ficher: H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A/Title: Isolation of CP(0)CP(1) from Chlamydomonas reinhardtii cw15 and the N-terminal A/Reference number: S68388; MUID:96128220; PMID:8543042
A/Molecule type: protein
A/Residues: 1-19 <FIEs.
A/Residues: 1-10 <FIEs.
A/Res
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; M; Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2525

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 < KUR>
A;Residues: 1-35 < KUR>
A;Residues: 1-35 < KUR>
A;Cross-references: UNIPROT:08YKC1; GB:BA000020; PIDN:BAB77138.1; PID:g17134579; GSPDB:G7Genetical Bource: strain PCC 7120
A;Genetical sar7380

A;Genome: plasmid
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16.4%; Score 31.5; DB 2; Length 35;
Best Local Similarity 40.7%; Pred. No. 1e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 13;
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A,Genome: nuclear
C,Keywords: chloroplast; hydrolase
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Best Local Similarity 40.0
Matches 6; Conservative
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Name-env;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Envelope glycoprotein (Fragment).
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                                                April 6, 2005, 13:10:34; Search time 180 Seconds (without alignments) 99.571 Million cell updates/sec
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34 AA.

PRT;

NCBI_TaxID=11676;

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"Molecular epidemiology of HIV transmission in a dental practice."; Science 256:1165-1171(1992).
                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Immunodeficiency virus type 1, viral sample FLQ5R3C (Florida local control 01), partial env cds, V3 region. (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92271245; PubMed=1589796; O. C.-Y., Clestelski C.A., Myers G., Bandea C.I., Luo C.C., C. Korber B.T.M., Mullins V.I., Schocherman G., Berkelman R.L., Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
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34 AA; 3786 MW; A93F03A44FAD828F CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00777; GP120.
InterPro; IPR00710; Ig-like.
Pfam; PF00516; GP120; I.
ADS; Coat protein; Glycoprotein; Transmembrane.
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                                                                                         Ida S., Garanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K., A. Kimura S., Iwamoto A., Oka S.;

"HIV type I V3 variation dynamics in vivo:long-term persistence of mon-syncytlum-inducing genotypes and translent presence of cyncytlum-inducing genotypes and translent presence of cyncytlum-inducing genotypes and translent presence of cyncytlum-inducing genotypes and is 1597-1609(1997).

Inducing genotypes during the course of progressive AIDS.";

AIDS Res. Hum. Retroviruses 13:1597-1609(1997).

Rembl. AB005321, Cantegral to membrane; IEA.

GO; GO:0019028; Cantegral to membrane; IEA.

GO; GO:0019028; Cantel capsid; IEA.

Red.; GO:0019028; Cantel experimental molecule activity; IEA.

InterPro; IPR007110; Ig-like.

Ref. Pfem; PP00516; GP120; I.
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MEDLINE=98090117; PubMed=9430252;
Midura S., Gatanaga H., Shicda T., Nagai Y., Kobayashi N., Shimada K.,
Kimura S., Iwamoto A., Oka S.;
Kimura S., Iwamoto A., Oka S.;
Thuring the course of progressive Airs.
Thuring anotypes during the course of progressive Airs.";
Thuring anotypes during the course of progressive Airs.";
AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
REMBL; AB005329; BAA33247.1;
REMBL; AB005329; C:viral capsid; IEA.
GO: GO:0019028; C:viral capsid; IEA.
R GO; GO:0019028; C:viral envelope; IEA.
R GO; GO:0019029; F:structural molecule activity; IEA.
InterPro: IPR00771; GP120.
R InterPro: IPR007110; Ig-like.
R Pfam; PPF00516; GP120; 1.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Score 46; DB 2; Length 34; Pred. No. 61; 5; Mismatches 6; Indels

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"Molecular epidemiology of HIV transmission in a dental practice."; Science 256:1165-1171(1992)
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11munodeficiency virus type 1, viral sample FLG5R3A (Florida local control 01), partial env cds, V3 region. (Fragment).

Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                  MEDLINE=92271245; PubMed=1589796; Ou C.-Y., Ciestelski C.A., Myers G., Bandea C.I., Luo C.C., Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L., Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W., Jaffe H.W.;
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11 SIPIGPGKAFYTTDIIGNI 29
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11 SIPIGPGRAPYTTNIIGNI 29

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"V3-loop and nef gene sequences of HIV-1 isolates from a hemophiliac cohort with long-term non-progressive infection.";
AIDS 13:532-534(1999).
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(APR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                              34 AA; 3818 MW; A93F02E148C0428F CRC64;
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               EMBL, AF082373; AAC3419.1; -. GO, GO:0016021; C:integral to membrane; IEA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:005198; F:structural molecule activity; IEA. InterPro; IPR00077; GP120. InterPro; IPR01005; Pept_S24_S26_C. Pfam; PF00516; GP120; I.
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                      Coat protein; Glycoprotein; Transmembrane
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Pred. No.
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11 SIPMGPGRAFYTTDRI 26
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Best Local Similarity
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Best Local Similarity
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A Ida S., Gatanaga H., Shloda T., Nagai Y., Kobayashi N., Shimada K., Kimura S., Iwamoto A., Oka S.;
Ida S., Gatanaga H., Shloda T., Nagai Y., Kobayashi N., Shimada K., Kimura S., Iwamoto A., Oka S.;
Inducing genotypes and transient presence of cyncytium-inducing genotypes during the course of progressive AIDS.";
AIDS Res Hum. Retroviruses 13:597-1609(1997).
R EMBL; AB005422; BAA3339-11, C.
R GO; GO:00190203; C.:integral to membrane; IEA.
GO; GO:00190203; C.:iral capsid; IEA.
GO; GO:0019011; C.:iral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
R InterPro; IPR001056; Pept_S24_S26_C.
R Pfam; PR00516; GP120.
M AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                            Exponence From Integral to membrane; IEA.

MEDILINE=98090117; PubMed=9430252;

A Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,

Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,

A Kimura S., Iwamoto A., Oka S.;

THU type 1 V3 variation dynamics in vivo:long-term persistence of

Ton-syncytium-inducing genotypes and translent presence of cyncytium-

Inducing genotypes during the course of progressive AIDS.";

AIDS Res. Hum. Retroviruses 13:1597-1609(1997).

Rembi, AB005421; BAA3338.1; -

Rembi, AB005421; BAA3338.1; -

Rembi, Colousous C: viral capsid; IEA.

GO; GO:0019021; C: viral capsid; IEA.

GO; GO:0019031; C: viral envelope; IEA.

Red); GO:00019038; F: structural molecule activity; IEA.

Retrovirus IPR000777; GP120.

Retrovirus Profice Colous Pept. S24. S26.C.
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AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Human immunodeficiency virus 1.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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43.8%; Pred. No. 87;
tive 5; Mismatches
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1es 7; Conservative
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InterPro, IPR010777, GP120.
InterPro, IPR011056; Pept_S24_S26_C.
Pfam; PP00516; GP120; Protein; Glycoprotein; Transmembrane.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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35 AA; 3718 MW; 9F53DAGE698BEB8C CRC64;
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35 AA; 3831 MW; 9F5A5B2A698BE26B CRC64;
  GO; GO:0005198; F:structural molecule activity; IEA
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBL_TaxID=11676;
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Local Similarity 36.0%; Pred. No. 1.2e+02,
les 9; Conservative 5; Mismatches 7;
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Pred. No. 1.2e+02;
3; Mismatches 3;
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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11 SIPIGPGRAFHTT 23
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Best Local Similarity
7; Conserve
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U66657; AAB58149.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
INTERPRO; IPR000777; GP120.
Pfam; PP001516; Pept_S24_S26_C.
Pfam; PP00516; GP120; 1.
AIDS; Coat protein; Glycoprotein; Transmembrane.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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11 SIPIGPGRAFYTTRQI 26
8 TLPVGPGPEFKTTLRV 23
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11 SIPIGPGRAFYTTRQI 26
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 250845; CAA90698.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                              loop (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11676;
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010869
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Matches

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Gaps

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"Antibodies of symptomatic human immunodeficiency virus type 1-
infected individuals are directed to the V3 domain of noninfectious
and not of infectious virious present in autologous serum.";
and not of infectious virious present in autologous serum.";
EMBL; Z15163; CAA78862.1;
GO; GO:0015621; Cintegral to membrane; IEA.
GO; GO:0019028; C:viral capsin IEA.
GO; GO:0019031; C:viral capsin IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 44; DB 2; Length 35; 53.8%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                        Schreiber M.G.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 AA; 3898 MW; 8A1B0F25558BF77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 AA; 3775 MW; 9F5B905B698BF77E CRC64;
                                                                                                                                                                                                                                                                                                                    GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019021; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
Interpro; IPR000777; GP120.
Interpro; IPR0101056; Pept_S24_S26_C.
Pfam; PP00516; GP120; 1.
AIDS; Coat protein; Glycoprotein; Transmembrane.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
V3 loop (Fragment).
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 1.2e+02;
4; Mismatches 4;
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InterPro; IPR011056; Pept S24 S26 C.
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22.9%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                          EMBL; Z50844; CAA90697.1;
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Matches 7; Conservative
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                                                       V3 loop (Fragment)
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                                       MEDLINE=98090117; PubMed=9430252;
A Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
A Kimura S., Iwamoto A., Oka S.;
Kimura S., Iwamoto A., Oka S.;
Kimura S., Iwamoto A., Oka S.;
Thy type 1 V3 variation dynamics in vivo:long-term persistence of non-syncytium-inducing genotypes and transient presence of cyncytium-inducing genotypes and transient presence of cyncytium-Inducing genotypes and transient presence of cyncytium-Inducing genotypes during the course of progressive AIDS.";
AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
REMBL; AB005440; BAA33356.1;
RGO; GO:0016021; Cintegral to membrane; IEA.
GO; GO:0016021; Cintegral to membrane; IEA.
GO; GO:0016031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
RO; GO:0019031; C:viral envelope; IEA.
RINTERPRO; IPR000777; GPIC.
RINTERPRO; IPR010056; Pept_S24_S26_C.
REPROSISE: REPROSI
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EMBL; AY305114; AAQ88346.1; -.
InterPro; IPR001777; FP120.
InterPro; IPR011055; Pept_S24_S26_C.
Pfam; PF00516; GP120; 1.
ANDS; Coat protein; Glycoprotein; Transmembrane.
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Pred. No. 1.2e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2; Length 35;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 AA; 4026 MW; 9E4A4A3A68BF77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6W884;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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53.8%;
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12 IPIGPGRAFYTTRQI 26
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Best Local Similarity 46.77
Conservative
7, Conservative
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Best Local Similarity 53.0.
7; Conservative
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11 SIPIGPGKAFYTT 23
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                     SEQUENCE PROM N.A.
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RESULT 14 076250 ID 07 AC 07 DT 01

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Search completed: April 6, 2005, 13:44:42 Job time : 181 secs

V3 loop p P24H/PRI p24E/V3 c Chimaeric

Aaw99973

Chimaeric

HIV-1 pep HIV-1 pep HIV-1 vac HIV-1 vac HIV-1 chim HIV-1 chim T1/V3 con T1/V3 con Chimaeric HIV-1 pep HIV-1 vac HIV-1 vac HIV-1 vac HIV-1 vac PIV EE15-

Aay39698 Aar38170 Aar38170 Aar38170 Aar38170 Aaw25840 Aaw25840 Aaw95940 Aaw99964 Aaw33972 Aay3972 Aay39765 Aaw99968 Aaw2309968 Aaw99968 Aaw21099

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This sequence represents the T-cell epitope derived from the HIV-1 core protein, T5, linked to a B-cell epitope, PRI which represents a consensus sequence derived from New York and Amsterdam HIV-1 isolates. Chimeric
                                                                                                                                                                                                                                                                                            T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope gag protein linked to B-cell epitope of V3 loop protein of an HIV-1 isolate.
                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                 19. .33
/label= T5
/note= "T cell epitope"
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/label= PRI
/note= "B cell epitope"
       AAY39698
AAR38170
AAR68170
AAR68670
AAW25840
AAW25840
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AAW39964
AAW39724
AAR68674
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AAR69666
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AAR21089
AAR21090
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                                                                                                                                                                                                                AAR68713 standard; peptide; 33 AA
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                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus
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(revised)
(first entry)
 PRI/T5 chimera, CLTB-159.
 CONNAUGHT LAB
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4444444444444444444444444
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25-MAR-2003
07-SEP-1995
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 AAR68713;
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Aaw25883 Chimaeric
Aaw98900 HIV-1 pep
Aay39728 HIV-1 pep
Aay39728 HIVI chim
Aar7763 PRI/T5 ch
Aaw6812 T5/PRI ch
Aaw67398 HIV-1 pep
Aaw98899 HIV-1 pep
Aay39727 HIV-1 pep
Aay39727 HIV-1 iso
Aay37762 T5/PRI ch
Aar7762 T5/PRI ch
Aar7766 HIV-1 iso
Aab1766 HIV-1 iso
Aab1766 HIV-1 iso
Aab1768 HIV-1 pep
Aaw5880 Chimaeric
Aab1768 HIV-1 pep
Aaw5880 Chimaeric
Aaw67396 HIV-1 pep
Aaw67396 HIV-1 pep
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PRI/P24H
Consensus
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HIV-1 env
HIV-1 V3
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                                                   6, 2005, 13:08:44; Search time 168 Seconds (without alignments) 80.575 Million cell updates/sec
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Compugen Ltd
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192
1 YEVHPYGTLPVGPGPEFKTTLRVQNLGCYVVSGLI
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                         2105692 segs, 386760381 residues
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        GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                      protein search, using sw model
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AAW67399
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AAW39727762
AAR77762
AAR68110706
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AAW25849
AAW67365
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Gapop 10.0 , Gapext 0.5
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length: 35
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Match
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Post-processing:

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Result Š

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The invention relates to new synthetic peptides comprising at least one amino acid sequence comprising an HIV gag protein T-cell epitope linked at the G- or N-terminus to an amino acid sequence comprising a B-cell epitope of the V3 loop of an HIV env protein, which can be used to generate vaccines against HIV-1. The T-cell epitope sequence is pref. selected from the T-halper determinant core peptides P24M, P24M, P24M, and P24H while the B-cell epitopes are derived from HIV strains including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIIB, RF, Z6, 2054, 1714 and BXOS The peptides are chimmeric and can be linked to a branched Lys backbone. This sequence represents a chimmeric peptide comprising the T-helper determinant core peptide TS (AAW25881) with the HIV-1 strain MN can by 1 loop B-cell epitope PRI (AAW25881) with the HIV-1 strain MN can be peptide generated from the consensus sequence of the New York and Amsterdam HIV-1 isolates. The B-cell epitope is linked to the N-terminus of the T-helper peptide. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                           ij
                These peptide sequences may also be used in the production of multimeric peptides in which the peptides are C-terminally modified by the addition of a Lys residue which is modified on its epsilon amino acid to carry an additional copy of the peptide molecule. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human or animal cells or by disturbing the 3D organisation of the virus. (Updated on 25-MMR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
  peptides such as this, may be used in the production of HIV-1 vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env; V3 loop; vaccine; determinant; chimaeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                Score 46; DB 2; Length 33;
Pred. No. 69;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimaeric T/B cell epitope peptide CLTB-159.
                                                                                                                                                                                                                                                                                                                                      SIPIGPGRAFYTTGYKYKVKIEPLG 30
                                                                                                                                                                                                                                                                                                                8 TLPVGPGPEFKTT----LRVQNLG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW25883 standard; peptide; 33 AA.
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.6%;
Matches 9; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-332082/30
                                                                                                                                                                                              Seguence 33 AA;
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22-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW25883;
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                                                                                                                                                                                                                                           Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                           Gaps
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  Length 33;
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  Score 46;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.0%; Score 46; 34.6%; Pred. No.
                                                                  SIPIGEGRAFYTTGYKYKVVKIEPLG 30
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                                                   ---LRVQNLG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 23-24; 40pp; English
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                                                                                                                                         AAW67399 standard; peptide; 33
                                                                                                                                                                                                                    HIV-1 peptide epitope CLTB-159.
                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                        95US-00464329
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24.0%;
ilarity 34.6%;
Conservative
                                                                                                                                                                                          (first entry)
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                                                   8 TLPVGPGPEFKTT---
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             Local Similarity
les 9, Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                  Synthetic.
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  Query Match
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               Best Loc
Matches
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the immunogenic composition of the invention. The composition comprises a synthetic fusion polypeptide which includes a sequence encoding 1 or more T cell epitopes and a sequence encoding 1 or more bettopes and a carrier. Both the T cell and B cell epitopes are derived from HIV proteins. The compositions are useful as vaccines against HIV infection. The composition induces HIV-1-specific polyclonal antibodies that are opsonising and antiviral. The peptide components may be selected to induce a response against different viral isolates and in subjects who recognise different T cell epitopes. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                    This sequence represents a fragment of a HIV1 protein, and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Modified at the epsilon N with a Lys residue which is substituted on the alpha and epsilon N with the sequence given in AAR68713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
                                                                                                                                                        Immunogenic composition containing synthetic fusion polypeptides containing both the T and B cell epitopes of the human immunodeficiency virus, useful antigens in producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%; Score 46; DB 2; 34.6%; Pred. No. 69; Live 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIPIGPGRAFYTTGYKYKVVKIEPLG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TLPVGPGPEFKTT----LRVQNLG 27
                                                                                                                                                                                                                                  Example 1; Col 25-26; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR77763 standard; peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1
                                                                                       Klein MH, Chong P, Sia CDY;
93US-00073378
94US-00257528
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/label= PRI
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/label= T5
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                                                     (CONN-) CONNAUGHT LAB LTD
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                                                                                                                        WPI; 1999-550482/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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09-JUN-1993;
09-JUN-1994;
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08-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a synthetic peptide comprising an amino acid sequence containing a T-cell epitope of an HIV gag protein linked a its C terminus to an amino acid sequence containing a B-cell epitope of an HIV gp41 protein and containing the amino acid sequence: XILKDWX2; where XI = E, A, G or Q, and X2 = A or T, or an amino acid sequence capable of eliciting an HIV-specific antiserum and recognizing the sequence XILKDWX2. The synthetic peptide is useful in vaccines against HIV infection and in diagnostic applications. AAW98892 to AAW9896, and AAW99899 to AAW99899 represent synthetic peptides from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope; infection; antibody; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic chimeric HIV polypeptides – comprising gag protein T-cell epitope linked to gp41 B-cell epitope.
                                                  HIV-1; human immunodeficiency virus, vaccine; T-cell epitope; gag protein; B-cell epitope; gp41 protein; chimeric; infection.
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                  HIV-1 vaccine synthetic peptide SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%; Score 46; DB
llarity 34.6%; Pred. No. 69;
Conservative 7; Mismatches
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                                                                                                                          Human immunodeficiency virus 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-189590/16
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26-NOV-1999
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                                                                                                                                                                                               12-MAR-1999
                                                                                                          Synthetic
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RESULT 5

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Gaps

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This sequence represents the T-cell epitope derived from the HIV-1 core protein, T5, linked to consesus B-cell epitope, PRI which represents a consensus sequence derived from New York and Ametradam HIV-1 isolates. Chimeric peptides such as this, may be used in the production of HIV-1 vaccines. These peptides say also be used in the production of HIV-1 multimeric peptides in which the peptides are C-terminally modified by the addition of a Lys residue which is modified on its epsilon amino acid to carry an additional copy of the peptide molecule. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human or animal cells or by disturbing the 3D organisation of the virus. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag protein T-cell epitope linked to env protein B-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env; V3 loop; vaccine; determinant; chimaeric.
                                                                                                                                                                            Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope gag protein linked to B-cell epitope of V3 loop protein of an HIV-I isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 45.5; Dilarity 34.6%; Pred. No. 81; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                            Claim 4; Page 46; 69pp; English.
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                    93US-00073378
                                                                                                Klein MH;
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(first entry)
                                                           (CONN-) CONNAUGHT LAB LTD.
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                                                                                                                                       WPI; 1995-036400/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 AA;
                    09-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
22-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5639854-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW25882;
                                                                                                Sia CDY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                         contains four opies a peptide monomer comprising the T-cell spitope derived from the HIV-1 core protein, T5, linked to the B-cell spitope, PRI which represents a commsensus sequence derived from New York and Amsterdam HIV-1 isolates. The entire multimer contains four copies of the same sequence linked through Lys residues. The B-cell epitope may be derived from HIV-1 proteins esp. 19160, agg and pol proteins. These chimeric peptides may then be used in the production of HIV-1 vaccines. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human called or by disturbing the 3D organisation of the virus. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
                                                                                                                                                                                                                                    Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of gag protein linked to B-cell epitope of V3 loop protein of an HIV-I isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           This sequence represents a multimeric lysine branched peptide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; Length 35;
Pred. No. 73;
7; Mismatches 4; Indels
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/label= PRI
/note= "B cell epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l. .15
/label= T5
/note= "T cell epitope"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TLPVGPGPEFKTT-----LRVQNLG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR68712 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                    Claim 4; Page 46; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
                                       94WO-CA000317.
                                                                                                                                                          Sia CDY, Chong P, Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-CA000317.
                                                                              93US-00073378
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Best Local Similarity 34.6%;
Matches 9; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                   (CONN-) CONNAUGHT LAB LTD.
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                                                                                                                                                                                                 WPI; 1995-036400/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003
25-MAR-2003
07-SEP-1995
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                                                                              39-JUN-1993;
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22-DEC-1994
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AAW98899 standard; peptide; 33
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34.6%;
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                                              Query Match
23.7%;
Best Local Similarity 34.6%;
Matches 9; Conservative
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Best Local Similarity 34.00.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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  Sequence 33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                       AAW98899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                             RESULT 10
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ID AAY3
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                 The invention relates to new synthetic peptides comprising at least one amino acid sequence comprising an HTV gag protein T-cell epitope linked at its C- or N-terminus to an amino acid sequence comprising a B-cell epitope of the V3 loop of an HIV env protein, which can be used to generate vaccines against HIV-1. The T-cell epitope sequence is pref. Selected from the T-helper determinant core peptides P24F, P24N, P24L, P24M and P24H while the B-cell epitopes are derived from HIV strains including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIIB, RF, Z6, 2054, T14 and BX08. The peptides are chimaeric and can be linked to a branched. Lys backbone. This sequence represents a chimaeric peptide comprising the T-helper determinant core peptide PRI which corresponds to a peptide conversion on protein V3 loop B-cell epitope PRI which corresponds to a peptide generated from the consensus sequence of the New York and Amsterdam HIV-1 strain M1 solates. The B-cell epitope is linked to the C-terminus of the T-helper beptide. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel immunogenic composition for use in vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes are generally designed based on the p24 core protein and the B-cell epitopes from the V3 loop of the gp120 protein from various HIV-1 extrains. This peptide corresponds to a fusion of the T5 epitope (AAMG7397) and the V3 loop Becall epitope (BAMG7365) which is a consensus V3 loop peptide of the New York and Amsterdam HIV-1 isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gpl20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 45.5; I 34.6%; Pred. No. 81; ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVHPYG-----TLPVGPGPEFKTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIEPLGVAPNTRKSIPIGPGRAFYTT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 23-24; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW67398 standard; peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1 peptide epitope CLTB-158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-00073378,
94US-00257528,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-556461/47
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 AA;
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AAW6

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AAW6

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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic chimeric HIV polypeptides - comprising gag protein T-cell epitope linked to gp41 B-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1; human immunodeficiency virus; vaccine; T-cell epitope; gag protein; B-cell epitope; gp41 protein; chimeric; infection.
                                                  7;
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Length 33;
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                                                  Indels
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                                                  s,
  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1 vaccine synthetic peptide SEQ ID NO:83.
                       Pred. No. 81;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 81;
Mismatches
     Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5;
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                                                                                                                              Example 1; Col 63-64; 41pp; English.
                                                                                                 EVHPYG-----TLPVGPGPEFKTT
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contains four opples a peptide monomer comprising the T-cell epitope derived from the HIV-1 core protein, T5, linked to the B-cell epitope, PRI which represents a commsensus sequence derived from New York and Amsterdam HIV-1 isolates. The entire multimer contains four copies of the same sequence linked through lys residues. The B-cell epitope may be derived from HIV-1 proteins esp. 19160, agg and pol proteins. These chimeric peptides may then be used in the production of HIV-1 vaccines. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human calls or by disturbing the 3D organisation of the virus. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS
                                                                                                                   /note= "Modified at the epsilon N with a Lys residue which is substituted on the alpha and epsilon N with the sequence given in AAR68712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of gag protein linked to B-cell epitope of V3 loop protein of an HIV-I isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a multimeric lysine branched peptide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus peptide RP150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 45.5; 34.6%; Pred. No. 86;
                             /label= T5
/note= "T cell epitope"
                                                                                                    'note= "B cell epitope'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVHPYG-----TLPVGPGPEFKTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein MH;
                                                                                                                                                                                                                                                                                                                                      94WO-CA000317
                                                                                                                                                                                                                                                                                                                                                                     93US-00073378
                                                                                  /label= PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    (CONN-) CONNAUGHT LAB LTD.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-036400/05
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35 AA;
                                                                                                                  Modified-site
                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                    08-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1993;
                                                                                                                                                                                                                                                                    WO9429339-A1
                                                                                                                                                                                                                                                                                                     22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2004
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sia CDY,
     Key
Peptide
                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a fragment of a HIVI protein, and can be used in synthetic fusion polypeptide which includes a sequence encoding 1 or more T cell epitopes and a sequence encoding 1 or more T cell epitopes and a sequence encoding 1 or more B cell epitopes and a sequence encoding 1 or more B cell epitopes and a proteins. The compositions are useful as vaccines against HIV infection. The composition induces HIV-1-specific polyclonal antibodies that are opsonising and antiviral. The peptide components may be selected to induce a response against different viral isolates and in subjects who standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic composition containing synthetic fusion polypeptides containing both the T and B cell epitopes of the human immunodeficiency virus, useful antigens in producing vaccines.
                                                                                                                HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope; infection; antibody; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.7%; Score 45.5; I Best Local Similarity 34.6%; Pred. No. 81; Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T5/PRI chimera lysine branched peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVHPYG-----TLPVGPGPEFKTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1, Col 25-26; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR77762 standard; peptide; 35 AA.
                                                                               HIV1 chimeric peptide CLTB-158
                                                                                                                                                                Human immunodeficiency virus 1
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                                                                                                                                                                                                                                                                   95US-00467881.
                                                                                                                                                                                                                                                                                                93US-00073378.
                                                                                                                                                                                                                                                                                                                                                                                     Sia CDY;
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB LTD.
                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-550482/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 AA;
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25-MAR-2003
08-SEP-1995
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                                                                                                                                                                                                                                                                                                                 09-JUN-1994;
                               17-OCT-2003
26-NOV-1999
                                                                                                                                                                                                 US5951986-A.
                                                                                                                                                                                                                                  14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                 Klein MH,
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AAY39727;
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17-AUG-2000
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Matches
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                                                                                                                                                                                                                                                                                       Peptide RPI50 comprises segments of the Principal Neutralising Domain (envelope protein) from isolate AVR-2. The last Cys residue is added for the purpose of crossfliking to carrier proteins. Cysteine residues may be added, so that the residues at or near both ends form a disulfide bond, giving peptide a loop-like configuration, which can be utilised to enhance the immunogenic properties of the peptides. Protein is capable of eliciting, and/or binding with, neutralising Abs. The neutralising domain is bounded by cysteine residues which occur at positions 296 and 331. Peptides can be used as immunogens or screening reagents to generate or identify poly- or monoclonal antibodies. See also ARR04427-R04506 and AAQ04273-Q0450. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viral protein; vaccine; anti-viral; anti-HIV; therapy; infection; gp120;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                            Principal neutralising domain of HIV variants - used for producing peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy therapy of HIV infection.
HIV isolate AVR-2; peptide RP150; principal neutralising domain; antibodies; diagnosis; prophylaxis; therapy; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                            Javaherian K, Farley J, Grimaila R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 isolate P1-932 gp120 protein V3 loop region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 2
Pred. No. 93;
3; Mismatches
                                                                                                                                                                                                                                                                       Claim 8 (81); Page 77; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB10706 standard; protein; 35 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
                                                                                           88US-00252949
                                                                                                               88US-00252949
                                                                                                                         89US-00359543
89US-00407663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.9%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.9
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                            Rusche JR, Putney SD,
Lynn DU, Petrobre J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                       (REPK ) REPLIGEN CORP
                                                                                                                                                                                                          WPI; 1990-147824/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 AA;
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                                                                                           3-OCT-1988;
                                                                                                                                   19-SEP-1989;
                                                                                                              03-OCT-1988;
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26-JAN-2001
                                                  409003984-A
                                                                                                                                                                                                                                                                                                                                                                                                                     field.)
                               Synthetic
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                                                                                                                                                                                                                                                                                                                           Viral vaccine comprises a mixture of protein sequence variants of a single viral protein, which is useful for prevention and therapy of viral infections, especially HIV, in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gpl20; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop; 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.9%; Score 44; DB 3; Length 35; 30.8%; Pred. No. 1.4e+02; Live 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1 V3-loop region (CXCR4-type) from isolate PI-932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VHPYGT----LPVGPGPEFKTTLRVQ 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG73686 standard; peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 79pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schreiber M, Seifert A, Meyer
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                                                                 99DE-01007485
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99WO-EP009759
                                                                                                                            (STRA-) STRATHMANN & CO AG.
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                                                                                                                                                                                                                                                                WPI; 2000-549084/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35 AA;
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03-DEC-1999;
                                                                 12-FEB-1999;
                                                                                                                                                                                              Schreiber M;
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11-MAR-2003
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Identifying compounds that modify interaction of gpl20 and co-receptors, useful potentially for treating human immune deficiency virus infection, also new peptides.
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Disclosure, Fig 2; 68pp; German.

This invention describes novel substances that modify the interaction between the gpl20 protein of human immunodeficiency virus (HIV), or its fragmants, with the co-receptors CXCR4, CCR5 and/or other 7-helix transmembrane receptors for HIV. The method comprises (a) immobilizing a ligand for the co-receptor on a gold surface; (b) contacting the ligand with suspended cells that express the co-receptor; and (c) determining interaction by measuring the refractive index (RI) by plasmon resonance. The procedure is repeated using cells that have been incubated with a test compound, and this is identified if RI is lower for cells for preincubated with a test compound, and this is identified if RI is lower for cells that includes the amino acid sequence of an HIV v3 loop (including flanking Cys). The products of the invention have virucide and anti-HIV and/or treatment of HIV infection. This sequence represents an HIV-1 v3-loop region described in the disclosure of the invention. (Updated on 29-NG-2003 to standardise OS field)

Sequence 35 AA;

1; Gaps 4. Query Match 22.9%; Score 44; DB 5; Length 35; Best Local Similarity 30.8%; Pred. No. 1.4e+02; Matches 9; Conservative 7; Mismatches 7; Indels

ठ 셤 Search completed: April 6, 2005, 13:41:36 Job time : 169 secs

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US-10-443-622-133
; Sequence 133, Application US/10443622
; Publication No. US20040024192A1
US-10-424-599-185421
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Sequence 133, App
Sequence 7462, Ap
Sequence 238025,
Sequence 172, App
Sequence 71, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208, App
Sequence 208, App
Sequence 208, App
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                                                                                        April 6, 2005, 13:44:50 ; Search time 139 Seconds (without alignments) 83.596 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 YEVHPYGTLPVGPGPEFKTTLRVQNLGCYVVSGLI 35
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US-10-443-622-133

US-10-10-66-698-7462

US-10-124-599-238025

US-10-125-865A-148

US-10-462-262-372

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US-09-864-761-46555

US-09-843-676-208
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US-10-053-758-208
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                                                                                                                                                                                                                                        1418010 segs, 331997259 residues
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                                                                                                                                              US-09-647-544-2_COPY_952_986
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
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                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                         Database
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                                                                                         Run
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Sequence 327, App
Sequence 127, App
Sequence 167, App
Sequence 167, App
Sequence 27, App
Sequence 27, App
Sequence 472, App
Sequence 472, App
Sequence 472, App
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Sequence 12, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 10828, A
Sequence 1083, A
Sequence 104, App
Sequence 105, Appl
Sequence 115, Appl
Sequence 293, Appl
Sequence 293, Appl
Sequence 293, Appl
Sequence 293, Appl
Sequence 284, Appl
Sequence 284, Appl
Sequence 285, Appl
Sequence 287, Appl
Sequence 287, Appl
Sequence 287, Appl
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Sequence 331, App
Sequence 3, Appli
Sequence 3, Appli
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4 US-10-054-295-208

4 US-10-054-611-208

4 US-10-054-611-208

4 US-10-054-611-208

5 US-10-310-810-327

6 US-09-798-889-167

6 US-09-798-889-167

6 US-09-913-767-472

7 US-09-913-767-472

4 US-10-004-860-472

4 US-10-004-860-472

4 US-10-004-860-472

4 US-10-004-861-10828

5 US-10-154-884B-10828

5 US-10-154-183

6 US-09-813-315

1 US-09-810-310-28

1 US-09-810-310-28

1 US-09-810-310-38

1 US-09-810-310-38
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Xovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 185421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13844C.1.pep
US-10-424-599-185421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.2%; Score 44.5; DB 15;
52.9%; Pred. No. 1.1e+02;
tive 3; Mismatches 4;
Sequence 185421, Application US/10424599; Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKTTLRVQNLG-CYVVS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || || || ::
10 YNTTARVDNLGDCYTLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
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Squence 238025, Application US/10424599
Fublication No. US20040031072A1
Fublication No. US20040031072A1
Fublication No. US20040031072A1
FUBLICANT: La Rosa Thomas J
APPLICANT: APOSTICANT: Thus Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SSQ ID NO 238025
LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stochl, Mark
APPLICANT: Stochl, Mark
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: DOLYBETIDES
TITLE OF INVENTION: DOLYBETIDES
TITLE OF INVENTION: DOLYBETIDES
CURRENT APPLICATION NUMBER: 60/284.534
PRIOR PILLING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_56963C.l.pep
US-10-424-599-238025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 15;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148, Application US/10125869A Publication No. US20030199671A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rondon, Isaac Jesus
APPLICANT: Wu, Qi-Long
APPLICANT: Ley, Arthur C.
          4 HPYGTL--PVGPGPEF 17
                                     11 HYFGKLVPPAGTGPEF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.9
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 PVGPGPEFKT 19
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ORGANISM: Glycine max
                                                                                                                                                  US-10-424-599-238025
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US-10-125-869A-148
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
RIOR PILING DATE: 1999-09-29
NUMBER: US 60/163,280
NUMBER: OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN VET: 3.0
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43.5; DB 15;
Pred. No. 1.1e+02;
4; Mismatches 6;
APPLICANT: Carrer et al.
TITLE OF INVENTION: 19 Human Secreted Proteins
FILE BEFRERCE : PZOO918
CURRENT APPLICATION NUMBER: US/10/443,622
CURRENT FILING DATE: 2003-05-23
FRIOR APPLICATION NUMBER: PCT/US99/13608
FRIOR APPLICATION NUMBER: 60/051,480
FRIOR APPLICATION NUMBER: 60/051,480
FRIOR APPLICATION NUMBER: 60/051,381
FRIOR APPLICATION NUMBER: 60/051,381
FRIOR APPLICATION NUMBER: 60/058,63
FRIOR APPLICATION NUMBER: 60/058,63
FRIOR APPLICATION NUMBER: 60/058,598
FRIOR APPLICATION NUMBER: 60/058,598
FRIOR APPLICATION NUMBER: 60/058,598
FRIOR APPLICATION NUMBER: 60/058,598
FRIOR FILING DATE: 1997-09-12
NUMBER: 60/050,598
FRIOR FILING DATE: 1997-09-12
NUMBER: 60/050,598
FRIOR FILING DATE: 1997-09-12
NUMBER: 60/050,598
FRIOR FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-10-106-698-7462
Sequence 7462, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 HPVSS-PEGPGPQYRGARR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 HPYGTLPVGPGPEFKTTLR 22
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Best Local Similarity 42.1
Matches 8; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-443-622-133
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 133
LENGTH: 28
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ORGANISM: artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/10/080,608A
CURRENT FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: human immunodeficiency virus type 1
Sequence 372, Application US/10462262
| Publication No. US20040009534A1
| GENERAL INFORMATION:
| APPLICANT: Satc, Aaron K.
| APPLICANT: Dawson, Bruce M.
| TITLE OF INVENTION: PROTEIN ANALYSIS
| FILE REFERENCE: 10280-052001
| CURRENT APPLICATION NUMBER: US/10/462,262
| CURRENT FILING DATE: 2003-06-16
| PRIOR PAPLICATION NUMBER: US 60/388,642
| RIGH FILING DATE: 2002-06-14
| NUMBER OF SEQ ID NOS: 430
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Xaa = Any Amino Acid US-10-080-608A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-080-608A-71
; Sequence 71, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VGPGPEFKTTLRVQNLGC 28
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YEVHPYGTLPVGPGPE 16
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LOCATION: 14
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICANT: Glidhers, Menrik Nerk K APPLICANT: Globbers, Edward B TITLE OWN: AND APPLICANT AND APPLICANTS NAME: ADDITION ADDITION APPLICANTS NAME: ADDI
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Gaps
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EXPRESSED IN BT474, SIGNAL = 1.9
EXPRESSED IN PLACENTA, SIGNAL = 1.1
EXPRESSED IN HBL100, SIGNAL = 1.9
EXPRESSED IN HBL100, SIGNAL = 1.2
EXPRESSED IN HBLA, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 1
EST_HUMAN HIT: AL121516.1, EVALUE 8.00e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
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TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
ZIP: 9411
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00069
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NO 45555
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 9; I
Pred. No. 3.4e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAP TO AC009973.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 208, Application US/09843676; Patent No. US20020164786A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVHPYGTLPVGPGPEFKTT 20
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.9°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MOTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-843-676-208
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EST_HUMAN HIT: H87835.1, EVALUE 2.00e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.3%; Score 39; DB 9; Length 20;
58.3%; Pred. No. 3.38+02;
iive 1; Mismatches 4; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-05-0
PRIOR APPLICATION NUMBER: WS 60/234,687
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PRIOR PILING DATE: 2000-06-30
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OTHER INFORMATION: MAP TO AC005747.1
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 HPYGTLPVGPGP 15
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ORGANISM: Homo sapiens
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Gaps
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Lingmer, Joachim
Lingmer, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPA: DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

TAPPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFTCATION BATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 10;
Pred. No. 3.8e+02;
0; Mismatches 5;
                                  PILING DATE: 25-APR-1997
CLASSIPICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/44,419
PILING DATE: 18-APR-1997
CLASSIPICATION NUMBER: US 08/724,643
PRIOR APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 136,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPAK: (415) 576-0300
TELEPAK: (415) 576-0300
TELEPAK: (415) 576-0300
TELEPAK: (415) 576-0300
TELEPAK: 72 amin, aride
                        US 08/846,017
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; Publication No. US20030032075A1
; GENERAL INFORMATION:
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58.3%;
       (IOK AFFALA....
APPLICATION NUMBER: US UN
PTI-ING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide
US-09-438-486-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-053-758-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
KORRESPONDENCE ADDRESS:
ADDRESSER: Twonsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
CITY: San Francisco
STATE: California
CCUNTRY: United States of America
ZIP: 94111-3834
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDRER: US/09/438,486
                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REPERRENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                        APPLICATION NUMBER: US/09/843,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-843-676-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEG ID NO: 208:
SEQUENCE CHARACTERISTICS.
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
                                              FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3°
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 HPYGTLPVGPGP 15
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US-09-438-486-208
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Gaps

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 18-Jan-2002
CLASSIFCATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                 Indels
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REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                  20.3%; Score 39; DB 14;
58.3%; Pred. No. 3.8e+02;
iive 0; Mismatches 5.
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FILING DATE: «UDKNOWN»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
COUNTRY: United States of America
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-054-295-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208, Application US/10054611

Publication No. US20030059787A1

GENERAL INFORMATION:
APPLICANT: Cach, Thomas R.
Ingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                     TELECOMMUNICATION INFORMATION TELEPRONE: (415) 576-020 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERIFICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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COUNTRY: United States of America
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.3%; Score 39; DB 14; Length 23; 58.3%; Pred. No. 3.8e+02; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Uhrboun»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 208:

US-10-053-758-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                  LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 HPYGTLPVGPGP 15
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US-10-054-295-208
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SIPIGEGRAFYTTGYKYKVKIEPLG 30
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Best Local Similarity 34.6%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single;
TOPOLOGY: linear
US-08-257-528B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
US-08-257-528B-84
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                                                                                                                         6, 2005, 13:32:19; Search time 42 Seconds
(without alignments)
62.208 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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TEVHPYGTLPVGPGPEFKTTLRVQNLGCYVVSGLI 35
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US-08-460-602A-84
US-08-465-217A-84
US-08-465-207A-84
US-08-467-801A-84
US-08-467-801A-84
US-08-141-833-11
US-08-141-833-11
US-08-467-858B-83
US-08-460-602A-83
US-08-460-602A-83
US-08-460-602A-83
US-08-461-2507A-83
US-08-461-2507A-83
US-08-461-2507A-81
US-08-461-2507A-81
US-08-461-2507-81
US-08-461-2507-81
US-08-465-217A-81
US-08-465-217A-81
US-08-465-217A-81
US-08-465-217A-81
US-08-465-217A-81
US-08-461-329A-81
US-08-465-217A-81
US-08-465-217A-81
US-08-467-881A-81
US-08-467-881A-81
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US-08-460-602A-81
US-08-465-217A-81
US-08-464-329A-81
US-08-467-329A-81
US-08-467-881A-81
US-08-457-8288-50
US-08-463-366A-50
US-08-463-366A-50
US-08-463-366A-50
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                                                                                                                                                                                                 US-09-647-544-2_COPY_952_986
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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| length: 35
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Maximum DB seq
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APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: TCHEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                              US-08-467-881A-50
US-08-513-968-71
US-08-513-968-71
US-08-257-528B-41
US-08-460-602A-81
US-08-460-602A-81
US-08-465-217A-41
US-08-465-217A-81
US-08-464-329A-41
US-08-464-329A-41
US-08-464-329A-81
US-08-464-329A-81
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Pred. No. 8.7;
7; Mismatches
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US-08-465-217A-84

Sequence 84, Application US/08465217A

Sequence 84, Application US/08465217A

Patent No. 5800822

GENERAL INFORMATION:
APPLICANT: GHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
CITY: Toronto
STATE: Ontaxio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
 COUNTRY: CALIBAGE
ZIP: MSG 1R7
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION UNMBER: 24,973
RIEDERRUGE/ACENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
TENDERME FRANCERENTSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB : Pred. No. 8.7; 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.6%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
Canada
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                   Sequence 84, Application US/08463966A
Patent No. 5795955
RENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
GITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TLPVGPGPEFKTT----LRVQNLG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELBEAK: (416) 595-1163
INFORMATION FOR SEQ ID NO: 84,
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 9; Conserva
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US-08-460-602A-84
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                                                                                                                                                                                                                                                             RESULT 6
US-08-462-507A-84
; Sequence 84, Application US/08462507A
; Patent No. 5876731
; GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
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                                                                                                                DB 2;
                                                                                                             24.0%; Score 46; DB 2
34.6%; Pred. No. 8.7;
tive 7; Mismatches
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NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10,77
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 33 amino acids
amino acid
                                                                                                                Query Match
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
     single
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Best Local Similarity
; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-464-329A-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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US-08-467-881A-84
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Patent No. 581754
GENERAL INFORMATION:
APPLICANT: GLONG, Pele
CORRESPONDENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
CITY: COCOMPTR: Canada
ZIP: MGG 1R7
COMPUTR: READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTR: IBM PC Compatible
COMPUTR: READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTR: BREADMELE FORM:
APPLICATION DATA: 87-108/844,329A
FILING DATE: 05-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 05-JUN 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 24,933
FILING DATE: 09-JUN 1993
CLASSIFICATION NUMBER: 24,933
FILING DATE: 09-JUN 1993
TELECOMMUNICATION NUMBER: 24,933
FILING DATE: 09-JUN 1993
CLASSIFICATION NUMBER: 24,933
FILING DATE: 09-JUN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%; Score 46; DB 1; Length 33; 34.6%; Pred. No. 8.7; tive 7; Mismatches 4; Indels
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                         APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
                                           FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 1038
TELECOMUNICATION INFORMATION:
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-465-217A-84
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                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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| Sequence 83, Application US/08257528B |
| Patent No. 563984 |
| Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038-336 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.7%; Score 45.5; D
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 46;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVHPYG-----TLPVGPGPEFKTT 20
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; Sequence 83, Application US/08460602A
; Zetent No. 5759769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::||| |:|| |:|
11 SISIGPGRAFRTTQIVGNL 29
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EARLIER FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                         NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-141-833-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , TOPOLOGY: linear
US-08-257-528B-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
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APPLICANT: OFFORD, ROBIN E
APPLICANT: THOMPSON, DARREN
APPLICANT: THOMPSON, JUL
TITLE OF INVENTION: N-TERMINAL MODIFICATIONS OF RANTES AND METHODS OF USE
FILE REFERENCE: GRPN-026/03US
CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: 60/056,292
EARLIER APPLICATION NUMBER: 60/056,292
EARLIER PILLING DATE: 1998-03-33
EARLIER FILLING DATE: 1998-03-33
EARLIER FILLING DATE: 1998-03-13
EARLIER FILLNG DATE: 1998-03-13
EARLIER PILLNG DATE: 1998-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      STRET: Suite /ul, 330 universely contact of STATE: Oncario country: Canada ZIP; MSG 1R7

COUNTRY: Canada ZIP; MSG 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATIOR SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,881A FILING DATE: 06-JUN-1995

CLASSIFICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994

PRIOR APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1993

CLASSIFICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993

CLASSIFICATION NUMBER: 24,973

FILING DATE: 09-JUN-1993

CLASSIFICATION NUMBER: 24,973

RESTRENCE/DOCKET NUMBER: 1038-488 MIS:jb

TELEFONMUNICATION NUMBER: 24,973

REFERENCE/OCKET NUMBER: 1155

TELEFONMUNICATION NUMBER: 24,973

REFERENCE/OFFITING NOMBER: 24,973

REFERENCE/OFFITING NOMBER: 24,973

REFERENCE/OFFITING NOMBER: 24,973

TELEFONMUNICATION NUMBER: 24,973

TELEFONMUNICATION NUMBER: 24,973

TELEFONMUNICATION NUMBER: 24,973

TELEFONMUNICATION NUMBER: 24,573

TELEFONMUNICATION NUMBER: 24,573
                             PREMENT NO. 591986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%; Score 46; DB 34.6%; Pred. No. 8.7; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TLPVGPGPEFKTT----LRVQNLG 27
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Sequence 84, Application US/08467881A
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Patent No. 6168784
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Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-467-881A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-141-833-11
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Sequence 83, Application US/08465217A

Patent No. 5800822

GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Anothel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEGUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
                                    PatentIn Release #1.0, Version #1.25
                                              SOFTWARE: PATENTIN RELEASE #1.0, VERBION #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-UUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/277,528
FILING DATE: 09-UUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE (416) 595-1155
TELEFRANCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELEFRANCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
23.7%; Score 45.5; D
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches
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FILING DATE: 09-UNW-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
            OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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US-08-463-966A-83
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Sequence 83, Application US/08463966A

GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTOR: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                      STREET: SULLE 'OL, CONTROLE OF TAYER: CONTROLE OF STATE: Oncario COUNTRY: Toronto STATE: Oncario COUNTRY: Canada ZIP: MSG 1R7

COMPUTER: ELABABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,602A FILING DATE: 02-UN-1995
CLASSIFICATION 0424
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/257,528
FILING DATE: 09-UN-1994
CLASSIFICATION NUMBER: 08/073,378
FILING DATE: 09-UN-1993
CLASSIFICATION NUMBER: 24,973
REPERBARE/AGENT INFORMATION: NAME: STEMARY INFORMATION: NAME: STEMARY INFORMATION: NAME: STEMARY INFORMATION: TELECOMMUNICATION POR SEQ ID NO: 83: SEQUENCE CHARACPERISTICS: TWATTH: TWATTH. 33 amino acids
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
CORRESPONDENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EVHPYG-----TLPVGPGPEFKTT 20
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STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.07
Then 9; Conservative
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-460-602A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-463-966A-83
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                                                                                                                                                                                                                                                                                                         Sequence 83, Application US/08462507A
Fatent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET Soute 701, 330 University Avenue
CITY: Toorato
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FLODPY disk.
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
PILNG DATE: 09-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILNG DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION NUMBER: 1038-451 MIS:jb
                                                  5.
               34.6%; Pred. No. 10; tive 5; Mismatches
                                                                                                        2 EVHPYG-----TLPVGPGPEFKTT 20
                                                                                                                                                                 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVHPYG-----TLPVGPGPEFKTT 20
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Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
               Best Local Similarity 34,69
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 amino acids
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Matches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83, Application US/08464329A
| Sequence 83, Application US/08464329A
| Patent No. S417754
| GENERAL INFORMATION:
| APPLICANT: SIA, Charles D.Y. APPLICANT: SIA, Charles D.Y. APPLICANT: CLEIN, Michel H.
| TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides UNMBER OF SEQUENCES: 101
| CORRESPONDENCE ADDRESS: ADDRESSE: Sim & McBurney STREET: Suite 701, 330 University Avenue CITY: Toronc CITY: Toronc CITY: Toronc CITY: Toronc COUNTRY: Canada ZIP: MSG 187
| COMPUTER: BMSG 187
| COMPUTER: BMSG 187
| COMPUTER: BM PC compatible COMPUTER: Ploppy disk COMPUTER: Ploppy disk COMPUTER: Ploppy disk COMPUTER: Plan PC compatible COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,329A FILING DATE: 09-JUN-1994
| PRIOR APPLICATION: 424 |
| PRIOR APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
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                                                                           1038-486 MIS: jb
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NAME: STEWART, MICHAEL 1. REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1163
TELEPHONE: 31 and 100 acide
TYPE: and 100 acide
TYPE: and 100 acide
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TYPE: and 100 acide
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NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/POCKET NUMBER: 1038
TELECHONE: (416) 595-1155
TELEPHONE: (416) 595-1156
INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.61
Matches 9; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     , TOPOLOGY: linear
US-08-465-217A-83
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US-08-464-329A-83
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us-09-647-544-2_copy_952_986.closed.rai

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DB 2; Length 33;
APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STRATE: Onteatio
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALORICATION ATA.
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: 09/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
APPLICATION: WAMBER: 09/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATCRNEY/AGENT INFORMATION:
APPLICATION NUMBER: 09/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATCRNEY/AGENT INFORMATION:
TELEPRAM: (416) 595-1155
TELECOMMUNICATION INFORMATION:
TELEPRAM: (416) 595-1165
TELECOMMUNICATION INFORMATION:
TELEPRAM: (416) 595-1165
TTELECOMMUNICATION OCIDS
SEQUENCE CHARATERISTICS:
LENGTH: 33 amino acids
TYPE: animo acids
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Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches
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g

2 EVHPYG-----TLPVGPGPEFKTT 20

Gaps 7;

Indels

Search completed: April 6, 2005, 13:45:31 Job time: 43 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein April Run on:

6, 2005, 14:42:11; Search time 43 Seconds (without alignments) 49.227 Million cell updates/sec

US-09-647-544-7

114 1 KLGFFAHKKIPEEEKREEKLEQ 22 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

4267

Minimum DB seq length: 0 Maximum DB seq length: 22

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

4:61 PIR Database :

1: pirl: * 2: pirl: * 3: pir2: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	valine-tRNA ligase	neurofilament heav	enamelin, 26K - bo	cytochrome-c oxida	cytochrome-c oxida	Ca2+-transporting	plastoquinol-plast	alkaline phosphata	hypothetical prote			_		ubiquitin carboxyl	ribosomal protein	sulfite reductase	insulin-like growt	caldesmon - turkey	2-aminobenzoate-Co	chromogranin-B - r	photosystem I chai	cytochrome-c oxida	alanine dehydrogen	motilin - dog (ten	cytochrome-c oxida	alkanal monooxygen	neural surface pro	protein T17H7.9 [i	nucleolin - bovine
SUMMARIES	ΩI	A49725	153671	S10786	843627	S65385	164832	PA0041	S13898	G83975	A61220	S11416	S36891	E33178	PC7043	F33084	PC4388	JH0517	A35552	539845	D49164	S06149	S77983	PX0078	S00189	S65392	B44995	A37968	H86433	802808
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	Query Match Length	19	20	17	20	10	8	15	16	17	18	20	15	18	21	22	22	16	16	18	20	20	20	21	22	14	18	19	22	19
æ	Query	35.1	26.3	25.4	25.4	24.6	23.7	23.7	23.7	23.7	23.7	23.7	ď.	22.8	22.8	ς.		Η.	ä	ä		21.9	21.9		21.5	21.1	21.1	21.1	21.1	20.6
	Score	40	30	29	29	28	27	27	27	27	27	. 27	56	26	26	26	56	25	25	25	25	25	25	2	24.5	24	24		24	23.5
	Result No.	1	8	Э	4	Ŋ	Q	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21			24	25	26	27	28	29

myosin heavy chain	hypothetical prote	shikimate 5-dehydr	ferredoxin b - Jap	ribosomal protein	lectin, galactose/	photosystem I chai	globin - polychaet	ribosomal protein	ribosomal protein	ribosomal protein	fucosyltransferase	fucosyltransferase	apolipoprotein E -	cytochrome-c oxida	beta-conglycinin a
A49018	C37765	I40062	869166	JP0070	A31516	806150	S19618	S78416	JP0071	C64330	S78007	S48196	A05310	S43625	816335
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23 2	23	23	23	23	23	23	23	23	23	23	23	23	22.5	22	22

ALIGNMENTS

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valine-tRNA ligase (EC 6.1.1.9) - rabbit (fragment)
N;Alternate names: valyl-tRNA synthetase
N;Alternate names: valyl-tRNA synthetase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dates: O3-May-1994 #sequence_revision 03-May-1994 #text_change 03-Jun-2002
C;Accession: A49725
R;Bec, G.; Kerjan, P.; Waller, J.P.
J. Biol. Chem. 269, 2086-2092, 1994
A;Title: Reconstitution in Vitro of the valyl-tRNA synthetase-elongation factor (EF) lbe lta subunit in complex formation.
A;Reference number: A49725; MUID:94124563; PMID:8294461
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A;Molecule type: protein
A;Residues: 1-19 <BEC>
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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Pred. No. 30;
4; Mismatches
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50.0%;
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2 QLPXEAKKNEKLEK 15
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Best Local Similarity 50.0°
Matches 7; Conservative
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RESULT 2

neurofilament heavy subunit - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 153671
R;Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.
Gene 132, 297-300, 1993
A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament hea A;Reference number: 153671; MUID:94040777; PMID:8224877
A;Accession: 153671
A;Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: mRNA A,Residues: 1-20 «RES» A,Cross-references: UNIPROT:Q16070; GB:S66488; NID:g452861; PIDN:AAB28609.1; PID:g452862

C; Genetics:

Length 20; Score 30; DB 2; I Pred. No. 7.1e+02; 1; Mismatches 5; A,Gene: GDB:NEFH A,Cross-references: GDB:120225, OMIM:162230 A,Map position: 22q12.1-22q13.1 26.3%; 53.8%; Query Match
Best Local Similarity 53.00
Best Local 7; Conservative

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Gaps

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5; Indels

9 KIPEEEKREEKLE 21

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Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
CiSpecies: Rattus norvegicus (Norvay rat)
CiSpecies: Rattus norvegicus (Norvay rat)
CiDate: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
CiAccession: I64832
R;Wu, K.
R;Wu, K.
A;Mu, Ehysiol. 264, 333-341, 1993
A;Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase is A;Reference number: I51892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C; Accession: PA0041
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
R; Kamo, Sparation, July 1994
A; Description: Separation and characterization of Arabidopsis proteins by two-dimensiona.
A; Reference number: PA0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alkaline phosphatase (BC 3.1.3.1) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13898
R;Fujimori-Arai, X.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.
Arch. Biochem: Bipphya. 1844, 320-325, 1991
A;Title: Purification and partial characterization of intestinal-like alkaline phosphatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plastoquinol-plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
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A;Residues: 1-15 <KAM>
A;Cross-references: UNIPROT:Q9ZR03; UNIPROT:Q94E14; UNIPROT:Q9FYB6
A;Experimental source: leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 2; Length 8; Pred. No. 2.8e+05; 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-8 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%;
57.1%;
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RVPDMEKR 15
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A, Status: preliminary
A, Molecule type: protein
                              9 KIPEEEK 15
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Best Local Similarity
Matches 4; Conserv
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C,Keywords: hydrolase
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C;Species: Rattus norvegicus (Norway rat)
C;Species: 12-Reb-1998 #sequence_revision 20-Reb-1998 #text_change 07-May-1999
C;Accession: 565385
R;Schaegger, H.; Moack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term A;Reference number: 865372; MUID:95324529; PMID:7601105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
CjSpecies: Salmo sp. (trout)
CjDate: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
CjAccession: 843627
RjFreund, R.; Kadenbach, B.
RjFreund, R.; Kadenbach, B.
Ajfitle: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrc AjReference number: 843624, MUID:94237150, PMID:8181469
AjAccession: 843624
                                                                                                                                           enamelin, 26K - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: 510786
R;Strawich, B.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth "enamelins" identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: 510780; MUID:90336641; PMID:2379503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <FRE>
C;Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory
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Pred. No. 6.7e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.4%; Score 29; DB 2; Length 17; 100.0%; Pred. No. 8.3e+02; Live 0; Mismatches 0; Indels
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Pred. No. 9.7e+02;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: protein
A, Realdues: 1.17 «STR»
A, Cross - references: UNIPROT: 07MZM6
C, Keywords: enamel; phosphoprotein
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Similarity 57.1%;
4; Conservative 3
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ilarity 40.0%;
Conservative
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4 KGIPTDEEQATGLEE 18
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Best Local Similarity 100...
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6 KSPEKAKSPEKEE 18
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A;Molecule type: protein
A;Residues: 1-10 <SCH>
C;Keywords: oxidoreductase
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
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R;Wittmann-Liebold, B.; Geissler, A.W.; Lin, A.; Wool, I.G.
J. Supramol. Struct. 12, 425-433, 1979
J. Supramol. Struct of the amino-terminal region of rat liver ribosomal proteins S4, S6, Sf A;Reference number: S11413; WUID:80252792; PMID:398910
A;Accession: S11416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CjAccession: S36891
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac.
A;Reference number: S36887; MUID:94009653; PMID:8405418
A;Accession: S36891
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R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.

Electrophoresis 11, 883-891, 1990

A;Title: Development of a database of amino acid sequences for human colon carcinoma pro-
A;Reference number: A33178; MUID:91176935; PMID:2079031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin carboxyl-terminal hydrolase (EC 3.1.-.-) homolog - yeast (Pichia anomala) (fra N,Alternate names: ALX1 protein
C,Species: Pichia anomala, Candida pelliculosa
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78K heat shock protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 23-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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Pred. No. 2.2e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              4; Indels
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                                                                                                                         A; Molecule type: protein
A;Reafdues: 1-20 «WIT»
A;Note: the protein is designated as ribosomal protein
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.8%; Score 26; DB 2; Le
ilarity 33.3%; Pred. No. 1.9e+03;
Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                              Score 27; DB 2; I
Pred. No. 1.8e+03;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein - Mycobacterium bovis (fragment)
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57.1%;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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1 AGEKAEKPDKKEQK 14
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Best Local Similarity 57.1
Matches 4; Conservative
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3 KNVPANSRRKAK 14
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Best Local Similarity
4; Conserva
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A;Molecule type: protein
A;Residues: 1-18 <WAR>
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A;Molecule type: protein
A;Residues: 1-15 <OHA>
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PC7043
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G8375
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Statuus: preliminary
A;Residues: 1-17 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-18 <MAT>
A;Cross-tefrences: UNIPROT:Q7M060
C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9K9N8; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB063 A;Experimental source: strain C-125 C;Genetics: A;Genet A;Genetics:
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Cispecies: Mus musculus (house mouse)
Cispecies: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
CiAccession: A61220
R Matsushita, S.; Katz, D.H.
Cill: Immunol: 137, 252-259, 1991
A;Title: The murine epsilon receptor modulating protein: a novel serine protease which: A;Reference number: A61220; MUID:91356570; PMID:1679381
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ribosomal protein L6, cytosolic [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C;Accession: S11416
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH2607 [imported] - Bacillus halodurans (strain C-125)
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Pred. No. 1.6e+03;
6; Mismatches 2; Indels
                                                                                                     DB 2; Length 16;
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                                                                                                  Query Match 23.7%; Score 27; DB 2; Best Local Similarity 83.3%; Pred. No. 1.5e+03; Matches 5; Conservative 1; Mismatches 0
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Pred. No. 1.5e+03;
2; Mismatches 5;
     A;Residues: 1-16 <FUJ>
A;Cross-references: UNIPROT:Q7M2K8
C;Keywords: phosphoric monoester hydrolase
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ilarity 33.3%;
Conservative 6
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50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
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KPAPKKEEKKKK 13
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Best Local Similarity
Matches 4; Conserva
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2 IPEEEE 7
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C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C;Accession: PC7043
K;Bakajo, 8.; Minagawa, N.; Yoshimoto, A.
Biosci. Biotechnol. Biochem. 63, 1889-1884, 1999
A;Title: Structure and regulatory expression of a single copy alternative oxidase gene :
A;Reference number: JC7145; MUID:20101471; PMID:1063554
A;Reference number: JC7145; MUID:20101471; PMID:1063556
A;Residues: 1-21 <SAK>
A;Residues: 1-21 <SAK<AX

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F33084
Indexident protein L18 - Haloferax mediterranei (fragment)
NyAlternate names: ribosomal protein HL13
C;Species: Haloferax mediterranei
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F33084
R;McDougall, J.
submitted to the Protein Sequence Database, June 1990
A;Reference number: A33084
A;McCession: F33084
A;Molecule type: protein
A;Residues: 1-22 <MCD>
A;Cession: P33084
A;Molecule type: protein
A;Residues: 1-22 <MCD>
A;Crose-references: UNIPROT:P50561
A;Reperimental source: strain DSM 1411
C;Superfamily: rat ribosomal protein L5
C;Keywords: protein biosynthesis; ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.8%; Score 26; DB 2; Length 21; 50.0%; Pred. No. 2.6e+03; tive 3; Mismatches 2; Indels
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Best Local Similarity 50.0
Matches 5; Conservative
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EDKREGEKEE 21
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Search completed: April 6, 2005, 14:59:35 Job time : 45 secs

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April 6, 2005, 14:40:45; Search time 174 Seconds (without alignments).
64.746 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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114 1 KLGFFAHKKIPEEEKREEKLEQ 22 US-09-647-544-7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

13872 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 22

Post-processing: Minimum Match 0% Maximum Match 100% Libting first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	s0 homo sapien	homo 88	gallu	gallus		_		y7 sus sp. ins		-	61 benincasa h	q3 homo sapien	z5 streptococc		87 oryctolagus				g8 bos taurus	60 mus musculu		_	42 crotalus at	_	malva	ednne	k0 homo sapien	s5 lepus timid			lepus
Desci	O8nes0	Q86wg4	Q91983	Q789b3	088660	Q16070	Q9r5u3	Q9try7	Q7m2m6	P80329	. P83961	©3ncd3	Q9r5z5	. Q78ed1	Q61ds7	Q9uci2	Q7m2k8	Q9k9n8	Q9trg8	Q7m060	015969	044710	P56742	Snjja2	P83137	. P16392	Q9ubk0	086185	Q86186	Q86187	086188
QI	QBNESO	Q86WG4	091983	Q789B3	039380	016070	Q9R5U3	Q9TRY7	Q7M2M6	COXF_ONCMY	BNCB_BENHI	<u>0</u> 900 <u>0</u> 3	Q9R5Z5	Q78ED1	Q6LDS7	Q9UCI2	Q7M2K8	Q9K9N8	Q9TRG8	090MLQ	Q15969	044710	OXLA_CROAT	Q9JJUS	AFP3_MALPA	GR78 HORSE	Q9UBK0	086185	086186	Q861 <i>S</i> 7	086158
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Q861S9 Q865Z8	Q86529 Q866A0	Q9R545 Q8HV61	O7RHL6	RL18 HALME	Q7RQ <u>9</u> 2	Q7S002	092766	MCA2 RHOOP	AF2S MALPA	IBP4_PIG
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ALIGNMENTS

RESULT 1

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	20 AA.			update)	lon update)				/ertebrata; Euteleo	Hominidae; Homo.					'DDBJ databases.				63A3A417E0B53F97 CRC64;	Score 33; DB 2; Length 20;	6e+03;	ss 2; Indels	
	20			ence	tat				a;	ini					ank,				E0B	٠.	-	tch	
	PRT;		Created)	Last sequ	Last anno	gment).			a; Craniat	s; Catarrh				Y.;	EMBL/GenB							u i	
	SO PRELIMINARY;	180;	01-OCT-2002 (TrEMBLrel. 22, Created)	CT-2002 (TrEMBLrel. 22,	CT-2002 (TrEMBLrel. 22,	MLL/CBL fusion protein (Fragment).	Name=MLL/CBL fusion;	Homo sapiens (Human).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	NCBI TaxID=9606;		SEQUENCE FROM N.A.	IF., Hsu JJ., Shih L	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.	EMBL; AY125965; AAM97173.1;	NON TER 1 1		SEQÜENCE 20 AA; 2323 MW;	Ouery Match 28.9%;	Best Local Similarity 46.2%:	6; Conservative	
00	Q8NES0	QBNESO;	01-0	01-0	01-0	MLL	Name	Homo	Euka	Mamm	NCBI	Ξ	SEOU	Fu	Subm	EMBL	NON	NON TER	SEOU	iry M	at Lo	Matches	
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RESULT 2

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Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI TaxID=9606;

[1]

SEQUENCE FROM N.A.

PubMed=14625809;

Leone P.E., Vega M.E., Jervis P., Pestana A., Alonso J.,

Paz-Y-Mino C.;

"Two new mutations and three novel polymorphisms in the RBI gene in Fundorian patients."; 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Retinoblastoma (RB1 protein) (Fragment). 16 AA. PRT; PRELIMINARY; Name=RB1; Q86WG4 Q86WG4;

Ecuadorian patients.

J. Hum. Genet. 48:639-641(2003). [2] SEQUENCE FROM N.A.

Gaps

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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[1]
SEQUENCE FROM N.A.
MEDLINE=89210285; PubMed=2707122;
MEDLINE=89210285; PubMed=2707122;
Lagrutta A.A., McCarthy J.G., Scherczinger C.A., Heywood S.M.;
Lidentification and developmental expression of a novel embryonic myosin heavy-chain gene in chicken.";
DNA 8:39-50(1989).
EMBL; MA4691; AA48950.1; -.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                   Score 31; DB 2; Length 19;
Pred. No. 2.8e+03;
0; Mismatches 3; Indels
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Pred. No. 2.6e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   SEQUENCE 19 AA; 2387 MW; 2DD5C6816CD4D6EC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IFA binding protein (spl0) (Fragment).
Brassica oleracea (Cauliflower).
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Last annotation update)
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EMBL; S66488; AAB28609.1; -.
PIR; IS3671; IS3671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.3%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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Q39380;
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                        Hogg A., Onadim Z., Baird P.N., Cowell J.K.;
"Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction sequencing.";
Oncogene 7:1445-1451(1992).
EMBL; AY243567; AA062758.1;
EMBL; L41913; AAA65748.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
MHC (19 AA) (Fragment).
MHC (19 AA) (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
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Pred. No. 1.7e+03;
4; Mismatches 5; Indels
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Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
EMBL; X06251; CAA29593.1; -.
PIR; S39082; S39082.
                                                                                                                                                                                                                                                                                                 16 AA; 1871 MW; 3A6A9791FD68E1E9 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Nucleic Acids Res. 15:8069-8085(1987)
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   MEDLINE=92319557; PubMed=1352398;
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1 KHLPGESKFQQKLAE 15
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Best Local Similarity 40.0%
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SEQUENCE
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Q91983,
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RESULT 3
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RESULT 4
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us-09-647-544-7.closed.rup

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"Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";

Eur. J. Blochem. 221:1111-1116(1994).
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-2004 (Rel. 44, Last annotation update)
Cytochrome oxidase polypeptide Vb-heart (EC 1.9.3.1) (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                Strawich E., Glimcher M.J.; "Tooth 'enamelins' identified mainly as serum proteins. Major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct protein sequencing; Inner membrane; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 17 17 SEQUENCE 17 AA; 2137 MW; FFA54E4CEE066720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AA; 2184 MW; 6A8E00CB33E92BD7 CRC64;
                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Enamelin, 26K (Fragment).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 2; Le
Pred. No. 4.7e+03;
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100.0%; Pred. No....
0; Mismatches
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                                                                                                                       PRT;
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PROSITE; PS00848; COX5B; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90336641; PubMed=2379503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94237150; PubMed=8181469;
                                                                                                                                                                                                                                                                                                                                                                                                                                     'enamelin' is albumin.";
Eur. J. Biochem. 191:47-56(1990)
PIR, S10786; S10786.
1
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Freund R., Kadenbach B.;
                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 HKKIP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 HKKIP 14
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                   Q7M2M6
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                                                                                RESULT 9
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Shimasaki S., Gao L., Shimonaka M., Ling N.;
"Isolation and molecular cloning of insulin-like growth factor-binding
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91358327; PubMed=1885526; Altenschaft U., Oswald B., Fuchs G.; Putinschaft U., Oswald B., Fuchs G.; Putilication and characterization of benzoate-coenzyme A ligase and 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor-binding protein-5, IGFBP-5 (Fragment).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
(VCBI_TaxID=9826;
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                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae.
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Pred. No. 4.8e+03;
2; Mismatches 4; Indels
                                                         Score 30; DB 2; Length 20;
Pred. No. 4.1e+03;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.3%; Score 30; DB 2; Length 22; 37.5%; Pred. No. 4.5e+03; ive 3; Mismatches 7; Indels
20 20
20 AA; 2198 MW; E9A0975B41FD8082 CRC64;
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20 AA; 2185 MW; F77C34A8FAA94EF9 CRC64;
                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                           22 AA.
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                                                                                                                                                                                                                                                                                                                                                                               2-amino-benzoate-CoA LIGASE=E2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 173:5494-5501(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Endocrinol. 5:938-948(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.9%;
                                                       Query Match 26.3%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                       9 KIPEEEKREEKLE 21
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Best Local Similarity
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas.
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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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"Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase isoforms in rat muscles.";
mm. J. Physiol. 264:333-341(1993).
EMBL; M99223; AA44092.1; -.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93273535; PubMed=8500915;

Gerlach D., Kohler W., Gunther E., Mann K.;

Gerlach and characterization of streptolysin O secreted by Streptococcus equisimilis (group C).";

Infect. Immun. 61:2727-2731(1993).

SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;
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Pred. No. 6.7e+03;
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Pred. No. 1.6e+06;
3; Mismatches 0; Indels
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                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus equisimilis.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D724140B1AAB076A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
Pred. No. 8.4e+03;
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                                                                                                                                                                                                                                                                                                                                                   15 AA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequenc
05-JUL-2004 (TrEMBLrel. 27, Last annotat
Calcium transporting ATPase (Fragment).
Name=SERCAlb;
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STRAIN-CD; TISSUE-Skeletal muscle;
MEDLINE-93191041; PubMed-8447366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Similarity 57.1%;
4; Conservative 3
                             66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |::| | ::|||
1 APKEMPLESAEKEEK 15
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Matches 7; Conservative
                                                              6; Conservative
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Best Local Similarity
Matches 4; Conserv
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PEDERRK 8
                             Best Local Similarity
                                                                                                                             13 EEKREEKLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
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Q78ED1
                                                           Matches
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STRAIN=Dong-gua; TISSUE-Seed;
STRAIN=Dong-gua; TISSUE-Seed;
STRAIN=Dong-gua; TISSUE-Seed;
SUBMEDIA: SECONDE DOTE: 0.016/S0196-9781(02)00271-1;
NG T.B., Parkash A., TSO W.W.;
"Purification and characterization of alpha- and beta-benincasins,
arginine/glutamate-rich peptides with translation-inhibiting activity
from wax gourd seeds.";
Peptides 24:11-16(203).
--- FUNCTION: Inhibits cell-free translation in rabbit reticulocyte
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benincasa hispida (Wax gourd).
Bukaryota, Viridiplannae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Cucurbitales, Cucurbitacese, Benincasa.
NCBI_TaxID=102211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Euthazia, Primates; Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lysate system.
-!- MISCELLANEOUS: IC(50) of 320 pM in rabbit reticulocyte.
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                          Score 29; DB 1; Length 20;
Pred. No. 5.6e+03;
4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UCQ3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
KU antigen 73 kDa protein fraction 31 (Fragment).
Homo sapiens (Human).
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Pred. No. 5.3e+03;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 45, Last sequence update)
05-JUL-2004 (Rel. 45, Last annotation update)
Beta benincasin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                 14 AA
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                             25.4%;
                                                           40.04;
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                                                           Best Local Similarity 40.0 Matches 6; Conservative
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Best Local Similarity
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6 EQERROER 13
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

Ca2+ ATPase (Fragment)

CA2+ ATPase (Fragment)

CA3+ ATPase (Fragment)

CA3+ ATPase (Fragment)

CA3+ ATPase (Fragment)

CA4+ ATPase (Fragment)

CA5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

CA5-JUL-2004 (
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Search completed: April 6, 2005, 14:55:45 Job time : 176 secs

11 PEEEKRE 17 ||:|:|: 3 PEDERRK 9

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ABP94458
ABP93790
ABP94825
                   ADO76553
AAU85588
ABU69560
ABU66463
ADH47375
ADJ21294
AAB99530
                                                AAB99524
       66688666767684644
(without alignments)
48.901 Million cell updates/sec
                      6, 2005, 14:41:35 ; Search time 174 Seconds
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                      114
1 KLGFFAHKKIPEEEKREEKLEQ 22
                protein search, using sw model
                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                   US-09-647-544-7
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ALIGNMENTS

AAB99533 AAY52610 AAB59148

AAW14811

740715

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 22

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseg 16Dec04: geneseqp1980s:* geneseqp1990s:*

Database

2105692 segs, 386760381 residues

Perfect score:

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protein

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Scoring table:

Lung canc Human lun Human lun Human Hsp Transcrip Alpha IIb Human Hsp Alpha IIb Hsp 708 II v-myb enc

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Abp94244
Abp94428
Abp94468
Abp94462
Adj32231
Adj32231
Adu6563
Abu69960
Abu69960
Abb7775
Adj21294
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Adj21294
Adh87375
Adj21294
Adh99530
Abb74746
Abb767474
Abb76767

prote

HLA I

Integrin alpha-10; ISa10; human; trauma; rheumatoid arthritis; osteoarthritis; osteoarthrosis; cancer; atherosclerosis; inflammation; therapy; cartilage; chondrocyte; osteoblast; fibroblast; vaccine; marker. Human integrin subunit alpha-10 cytoplasmic domain peptide. AAY32244 standard; peptide; 22 AA 98SE-00001164. 99SE-00000319. 99WO-SE000544. 15-FEB-2000 (first entry) BIOTECH AB Lundgren-Akerlund E; WPI; 2000-052639/04. (ACTI-) ACTIVE 31-MAR-1999; Homo sapiens W09951639-A1 02-APR-1998; 28-JAN-1999; 14-0CT-1999 AAY32244; RESULT 1 AAY3224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20008:* geneseqp20018:* geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:*

or inflammation.

Claim 21; Page 53; 90pp; English.

Aab59147 Alpha IIb
Aa448683 Amino aci
Ad227160 Human int
Abp94377 HLA prote
Abp94921 HLA prote
Abp94921 HLA prote
Abp95230 HLA prote
Abb95230 HLA prote
Abu65587 Lung tumo
Abu69559 Human lun
Abu6959 Human lun
Abu6959 Human lun
Ad121293 Human lun

AW46663 ADA21760 ADA217160 ABP943177 ABP9432104 ABP95230 ABP65587 ABU65587 ABU65587 ABU65587 ABU65587 ABU65587 ABU6558986 ABB20986

Polyanion Alpha IIb Integrin Alpha IIb

Abp56388 Aab59156 Aar88078

ABP56388 AAB59156 AAR88078

Aay32244 Human int

Description

08

Length

Query Match 1

Score

Result

This sequence represents a fragment of novel human chondrocyte integrin subunit alpha-10 (1Sal0, see AAY32242), corresponding to the C-terminal cytoplasmic domain of the protein. The invention relates to a recombinant or isolated integrin heterodimer comprising the alpha10 subunit in association with subunit beta (especially beta-1). The integrin heterodimer, or the subunit alpha-10, or a fragment of it such as the present sequence, can be used as a marker or target of all types of cells, e.g. of chondrocytes, osteoblasts and fibroblasts. They can also be used: for treating pathological conditions involving ISal0, such as damage to cartilage, trauma, rheumatoid arthritis or osteoarthritis; for

New isolated integrin subunit alpha-10, used as a marker or target molecule for cells during development, regeneration and pathological conditions, e.g. arthritis, osteoarthrosis, cancer, atherosclerosis

Peptide # Protein # Human bon

HLA prote HLA prote HLA prote HLA prote HLA prote

Abp93956 I Abp95368 I Abp94457 I

ABP93956 ABP95368 ABP94457

ABP94987

Aam68751 B Abp95115 B Abp94987 B

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Leukine, where the polyanionic polymer is polyglutamic acid or polyaspartic acid; (3) a vector (III) comprising a cassette which comprises a nucleotide sequence encoding a polyanionic polymer and at least one other nucleotide sequence, where the polyanionic polymer is polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell (IV) comprising (II) or a vector that comprises a nucleotide sequence that encodes a polyanionic polymer that is larger than 10 kDs, and (6) a recombinantly-produced polyanionic polymer (V) that is of any molecular weight or is larger than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or ailment in an individual by administering (I) to the individual. (I) is also useful for delivering an effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and testing or research purposes. AB2222045 to AB222131 and ABB56374 to ABB56400 represent sequences used in the exemplification of the present

88888888888888888888888888

Sequence 19 AA;

invention

polyanionic polymer (II) conjugate comprising a polyanionic polymer and

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                 physiological or therapeutic reparation of cartilage, or detecting regeneration of cartilage or chondrocytes during transplantation of cartilage or chondrocytes during transplantation of cartilage or chondrocytes; for selection and analysis or for sorting, disclating or purification of chondrocytes and for in vitro studies of differentiation of chondrocytes; and as a target for anti-adhesive drugs or molecules in tendon, ligament, skeletal muscle or other tissues where adhesion impairs the function of the tissue (all claimed). Isa10 binding entities can be used to determine the differentiation-state of calcel during embryonic development, anglogenesis or development of cancer, in pathological conditions such as rheumatoid arthritis, osteoarthrosis or
                                                                                                                                                                                  cancer, in tissue regeneration or in therapeutic and physiological reparation of cartilage (claimed). A vaccine comprising the integrin heterodimer or subunit alpha-10 is also claimed. 18310 polynucleotides, vectors, host cells and methods of producing recombinant ISal0 are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing monodispersed preparation of polyanionic polymer for therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the
                                                                                                                                                                                                                                                                                                                                                    Gaps
 detecting the formation of cartilage during embryonal development
                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tompkins CK;
                                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 3; Length 22; 100.0%; Pred. No. 5.7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyanionic polymer; bloactivity; water solubility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lofquist A, Pietz GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polyanionic polymer related peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                   KLGPFAHKKIPEEEKREEKLEQ 22
                                                                                                                                                                                                                                                                                                                                                                                                        1 KLGFFAHKKIPEEEKREEKLEQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP56388 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US008614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-0277705P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       مدسيط DW, Bergman PA,
Waggoner DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-058367/05.
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                                                                                                                                                                                                                                                                                   Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO200277036-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                           Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a peptide with a series of heptadrepats that mimic a transmembrane domain and a selected cytoplasmic domain attached to the heptad repeats. The invention is useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein with the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying a cytoplasmic domain binding partner. It is may be used to study protein interactions with transmembrane proteins such as integrin, which can be used to treat conditions in which over activity of integrins is involved,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to the repeats.
                                       Gaps
                                       .
    Length 19;
                                     2; Indels
         ;
9
      Score 44; DB 6
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                          Alpha IIb beta 3 binding motif peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 13; 36pp; English.
                                                                                                                                                                                AAB59156 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000WO-US014656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00320907
      38.6%;
57.1%;
                                                                                        9 KIPEEEKREEKLEQ 22
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                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsberg MH, Pfaff M;
                                                                                                                                                                                                                                                                                                                             thrombosis; malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-041143/05.
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         WO200073341-A1.
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                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                               RESULT 3
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The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than 10 kD. (M) involves inserting into an expression vector (EV) a ligation product formed by ligating together oligonucleotides that encode glutamate/aspartate residues, expressing EV in a host cell, and isolating the protein product (P) of EV, where (P) is PP and at least 80% of PP is approximately of the same molecular weight. Also described: (1) a recombinant fusion protein (I) comprissing a polyanionic polypeptide and another polypeptide at either one end or at both ends of it; (2) a

Matches

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transmembrane domain; cytoplasmic; integrin; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to the repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a peptide from the integrin beta-3-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; integrin beta-3-subunit; inhibition; cellular adhesion; cell adhesion regulatory domain; CARD; tumour; inflammatory refibroblast proliferation; coronary disease; vascular disease; respiratory distress syndrome; retinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 50;
                                                                     Alpha IIb beta 3 binding motif peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.7%; Score 43; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 13; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW48683 standard; peptide; 19 AA
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                                                                                                                                                                                                                                                                        26-MAY-2000; 2000WO-US014656.
                                                                                                                                                                                                                                                                                                         99US-00320907
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                                 (first entry)
                                                                                                                                                                                                                                                                                                                                             (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                          malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-041143/05.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
                                                                                                                                                                                              WO200073341-A1
                                                                                                       Heptad repeat;
thrombosis; ma
                                                                                                                                                                                                                                                                                                           27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                 Ginsberg MH,
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                                 21-MAR-2001
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                                                                                                                                                              Synthetic.
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BXBXGXGXGXGXGXGXG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88078 represents the human integrin alpha-IIb cytoplasmic domain. It is used to produce a Tac/integrin chimera having the cytoplasmic domain as above covalently linked to the extracellular and transmembrane domain of the Tac subunit of the human interleukin-2 receptor. Chimeric integrins can be used to block the activity of natural integrins in vivo. This provides an alternative route, to using small molecule inhibitors of ligand binding by integrins, of studying and modulating integrin activity in vivo. These inhibitors act on the interaction between intracellular molecules and integrins and are therefore likely to be cell type-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New soluble protein models of transmembrane receptors - have helical amphiphilic sequence to represent transmembrane domain, also chimeric integrin proteins for inhibiting human cellular integrins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Helical; soluble; amphiphilic; integrin; chimera; inflammation; inhibition; thrombosis; malignancy; transmembrane receptor.
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                                                                       Length 20;
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                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kent SBH,
such as inflammation, thrombosis and malignancy
                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2
Pred. No. 50;
2; Mismatches
                                                                DB
36;
                                                                                                         Mismatches
                                                                     Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 Integrin alpha-IIb cytoplasmic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 9; 100pp; English.
                                                                                                                                                                                                                                                                        AAR88078 standard; peptide; 20 AA
                                                                                                         2;
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50.0%;
                                                                     38.6%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muir TW, Williams MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-049670/05.
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                                   Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                               30-JUL-1996
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Gaps

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RESULT 5 AAB59147 ID AAB5 XX

ò 셤 Greene JM;

Wei Y,

Moore PA,

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The invention relates to an isolated nucleic molecule that is at least CC 95% identical to 18 human cDNA sequences representing 12 novel genes cenced proteins or a polymuclecide fragment of the cDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polymuclecide having a homologue, a variant or allelic variant of the polymuclecide capable of hybridising under conditions the polymuclecide, where the polymuclecide capable of hybridising under conditions the polymuclecide, where the polymuclecide conditions to a nucleic acid molecule companies under stringent conditions to a nucleic acid molecule capabinant vectors, host cells for producing the polympetide, the secreted polypeptide fragment, domain, epitope full-length protein, variant, allelic variant or species homologue), antibodies that secreted polypeptide fragment, domain, epitope full-length protein, variant of the polypeptides, diagnosing treating, preventing or ameliorating amedical condition by administering the polymuclectide or the polypeptide, the gene corresponding to the cDNA sequence and sequence in a cell, isolating the supernatant, and detecting an activity or in a biological seasy and identifying the protein in the supernatant or pathological condition, for preventing, treating, or ameliocating a condition, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune condition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for certicition mapping. The polypeptides and antibodies are useful for contrasses or decrease storage capabilities, fat contracts or other contrasses or decreases storage capabilities, and public proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit. The present sequence is the Integrin alpha cytoplasmic domain motif as found in the gene7 protein
                                                                                                                                                                                                                                                                                                                                                      New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 39; DB 6; Le 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 53; Page 257; 454pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI39445 standard; peptide; 7 AA.
                                                                                                                                                                                                                              Young PE, Kenny JJ, Ol
M, Liu D, Crocker PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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                                                                           WEI Y. GREENE J M.
KENNY J J.
OLSEN H S.
MOORE P A.
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Best Local Similarity
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                                                                                                                                                       LIU D.
CROCKER P.
                                                                                                                               RUBEN S M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                                                                                                                        Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders.
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                                                                                                                             (RUBE/)
(LIUD/)
(CROC/)
     KENN/)
                            OLSE/)
                                                    MOOR/
                                                                                                     GREE/
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     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of a peptide from human integrin beta-3-subunit, which is used in the method of the invention. This method shrotoves the inhibition of cellular adhesion, which the use of peptides comprising a cell adhesion regulatory domain (CARD) of an adhesion receptor abunit expressed by the cell. The method is useful in treatments requiring inhibition of cellular adhesion e.g. to prevent growth of tumours, since adhesion is required to form tumour masses. It can be used to inhibit cellular inflammatory responses, (especially when the CARD is an integrin beta or alpha subunit), and to the peptide comprises an integrin beta is CARD. The method is useful to treat excessive fibroblast proliferation (especially to heal wounds) when the peptide comprises an integrin beta is CARD. The method is useful to treat coronary and/or vascular diseases, as well as respiratory distress syndrome, and retinosis in the blood
                                                                                                                                                                                                                                                                             Inhibiting cellular adhesion useful e.g. to prevent tumour growth - by introducing peptide(s) comprising cell adhesion regulatory domain of an adhesion receptor or counter receptor sub-unit expressed by the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; preservative; secreted protein; integrin alpha; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%; Score 42; DB 2; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human integrin 10alpha subunit cytoplasmic domain motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 65;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                Example; Page 23; 76pp; English
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                          97WO-US018331.
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19-APR-2000; 2000US-0198407P.
30-0CT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836553.
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                                                                           96US-0028420P
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les 9; Conservative
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                                                                                                                                                                            Hawiger JJ, Timmons S,
                                                                                                                             UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                              WPI; 1998-251051/22.
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(YOUN/) YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003055231-A1
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                       09-OCT-1997;
                                                                           15-OCT-1996;
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RESULT 7 ADA27160

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Indels Length 7;

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09-APR-2002; 2002WO-US011359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                     The invention relates to a marker (I) for mammalian mesenchymal stem cells (MSC), comprising an integrin alpha10 and/or integrin alpha11 chain userpressed on cell surface of a MSC or intracellular in a MSC. (I) is useful for identification of a mammalian MSC, for modulating differentiation of a mammalian MSC, for solating a mammalian MSC is useful for identifying, differentiating and isolating amammalian MSC from a mixed cell population as useful tools in cell therapy or in repair of damage tissue. The present sequence represents a sequence from the integrin alpha10 cytoplasmic domain which is present in the place of a conserved integrin cytoplasmic domain motif (ADI39444).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                          Marker for mammalian mesenchymal stem cells, useful for identifying and isolating mesenchymal stem cells, comprising integrin alpha 10 and/or integrin alpha 11 chain expressed on surface or within the stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
humoral immune response; cellular immune response;
suppression subtractive hybridisation; HLA; human leukocyte antigen.
                                                MSC; mesenchymal stem cell; integrin alpha10; integrin alpha11; cell therapy; tissue repair; cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 39; DB 8; Length 7;
                              Integrin alphal0 cytoplasmic domain peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA protein 121P2A3 peptide #10732
                                                                                                                                                                                                                                                                                                    Disclosure, Page 2, 37pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP94377 standard; peptide; 15 AA.
                                                                                                                                                               14-JUN-2002; 2002SE-00001831.
                                                                                                                                            12-JUN-2003; 2003WO-SE000983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
         (first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                   Lundgren-Akerlund E;
                                                                                                                                                                                                                                       WPI; 2004-062518/06.
                                                                                                                                                                                             (CART-) CARTELA AB.
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                                                                                                   WO2003106492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200283068-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                               Unidentified
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         22-APR-2004
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                                                                                                                       24-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulat activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for cliciting humoral or callular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal course as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancercus tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP813646 - ABP95595 represent peptides from the 121P2A3 variants of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
                                                                                                                                                                                                                                                         Mitchell SC;
W, Jakobovits A;
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humoral immune response; cellular immune response;
suppression subtractive hybridisation; HLA; human leukocyte antigen.
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                                                                                                                                                                                                                                                         Challita-Eid PM, Raitano AB, Faris M, Hubert RS,
Afar DEH, Saffran D, Morrison K, Morrison RK, Ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 263; 362pp; English.
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10-APR-2001; 2001US-0282739P.
25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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25-APR-2001; 2001US-0286630P.
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versus cancerous tissues.
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ARGKLEEEKKRSEEL
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                                                                                                                                                                            (AGEN-) AGENSYS INC
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Mitchell SC;

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The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the modulates the status of a protein, 121P2A3. The composition of the invention has eytoetatic and immunostimulat activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for claracterising cytogenetic abnormalities of this chromosomal colours, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in the chromosomal region that encodes 121P2A3 that may contribute to comparating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP835646 - ABP95595 represent peptides from the 121P2A3 variants of the invention
                                                                                             New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
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Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
  ano AB, Faris M, Hubert RS, Mitchell SC;
Morrison K, Morrison RK, Ge W, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h Similarity 53.3%; Score 39; DB 6; Length 15; Similarity 53.3%; Pred. No. 1.4e+02; 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                               Claim 13; Page 274; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA protein 121P2A3 peptide #11585.
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  Raitano AB,
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25-APR-2001; 2001US-0286630P.
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1 ARGKLEEEKKRSEEL 15
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                                                                                                                                                         versus cancerous tissues.
                      Afar DEH, Saffran D,
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Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                         The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has extosette and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for caracterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities of in the chromosomal region that encodes 121P2A3 that may contribute to an alignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The pricing are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention
                                                                                                                                                                         New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
                                                                           id PM, Raitano AB, Faris M, Hubert RS, Mitchell SC; Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
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humoral immune response; cellular immune response;
suppression subtractive hybridisation; HLA; human leukocyte antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 39; DB 6; Length 15; 53.3%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                         Claim 13; Page 254; 362pp; English.
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                                                                             Challita-Eid PM, Raitano AB,
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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22-JUN-2001; 2001US-0300373P
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hes 8; Conservative
                                                                                                                                                                                                                                      versus cancerous tissues.
                                                                                                                                    WPI; 2003-092956/08
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                                      (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
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                                                                                               Afar DEH,
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ABP94921
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Gaps

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Bangur CS,
Clapper JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; lung
                                                                                                                                                                                                                                                                                                                                                                                             ABU69559;
                                           Claim 2;
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(FANG/)
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                                                                                                                                                                                                                                                                                                                                                                        modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polymucleotides are useful for eliciting humoral or cellular immunostimulatices. The polymucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83546 - ABP95595 represent peptides from the 121P2A3 variants of the invention
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                                                                                        The invention relates to a novel composition comprising a substance that
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         New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
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Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                        Score 39; DB 6; I
Pred. No. 1.4e+02;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung tumour protein L548S peptide #22.
                                                                  Claim 13; Page 280; 362pp; English
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2000US-00658824.
2000US-00671325.
                                                                                                                                                                                                                                                                                                                         34.2%;
53.3%;
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2000US-00736457
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1 ARGKLEEEKKRSEEL 15
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                                             versus cancerous tissues.
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                                                                                                                                                                                                                                                                                                    Sequence 15 AA;
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06-OCT-2000;
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13-DEC-2000;
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                                                                                                                              The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated peptide. This patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; lung tumour; cytostatic; vaccine; T cell expansion;
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Novel polymucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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Pred. No. 1.8e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published pct_sequences
                                                                                 SEQ ID NO 1855; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU69559 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2000; 2000US-00736457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
7; Conserve
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WANG T.
SWITZER A F
MCNEILL P CLAPPER J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
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the specification, or a sequence (S2) mentioned in specification, or a sequence service (S2) mentioned in specification, or a sequence consisting of at least 20 contiguous residues of S1, sequences having 75%, preferably cof S1, sequences har hybridise to S1, sequences having 75%, preferably cof S1, sequences har hybridise to S1. Also included are an isolated polypeptide (comprising a sequence (S3) selected from any one of the 4 maino acid sequences mentioned in the specification, a sequence moded by the polymorlectide, or sequences having at least 70%, preferably 90%, identify to a sequence encoded by the polymorlectide, an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that the vector, an isolated antibody (or its antigen-binding fragment) that the operation control sequence, a host cell transformed or transfected with the operations, attainable to an appecifically binds to the polypeptide, detecting the polypeptide, an expression control sequence, a host cells specific for a tumour conditions, etimulating and/or expanding T cells specific for a tumour or antigen-presenting cells, under conditions and for a time sufficient comprising contacting T cells with the polymorlectide, protein contacting cells, under conditions and for a time sufficient contacting cells that express the polymorlectide, such that T cells for expanding to the patient with the polymorlectide, protein or antigen presenting cells that express the polymorlectide, such that T cells for presenting cells that express the polymorlectide, such that T cells composition for simulating an immune response in a patient, and for the patient the presence of a cancer in a composition for simulating an immune response in a patient, and thus immune response to the patient. The protein and oligomorlectide is also useful in pharmaceutical compositions, e.g. vaccines. The polymorlectide is a sequence of a cancer in a patient per presence of a cancer in a patient per 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library. The present sequence is an epitope mapping peptide derived from the cDNA L548S isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
a sequence selected from any of the 14 sequences mentioned in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the USPTO at segdata.uspto.gov/sequence.html?DocId=20020197669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 39; DB 6; Length 20;
53.8%; Pred. No. 1.8e+02;
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer therapyand diagnosis associated protein #86.
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Best Local Similarity 53.8
Matches 7; Conservative
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10-JUL-2001; 2001US-00902941.

99US-00346492.

30-JUN-1999; 15-OCT-1999;

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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polypeptide associated with the compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                                                                                                                       New polynucleotide, useful for preparing a composition for treating or inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                     Mcnabb A;
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                                                                                                                                                                                                                                         (, Johnson JC, Retter MW;
Vedvick TS, Bangur CS, M
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                                                                                                                                                                                                                                         Watanabe Y,
                                                                                                                                                                                                                                                       Fanger GR,
                                                2000US-00546259.
2000US-00560406.
2000US-00589184.
2000US-00614124.
2000US-00651563.
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2000US-00677419.
2000US-00702705.
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2001US-00849626
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Carter D, F
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Matches 7; Conserv
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                                                  10-APR-2000;
27-APR-2000;
05-JUN-2000;
11-JUL-2000;
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                                                                                                      29-AUG-2000;
08-SEP-2000;
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03-MAY-2001;
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                                                                                                                                                                                                                                                     Durham M,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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April 6, 2005, 14:58:57; Search time 138 Seconds (without alignments) 52.927 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-647-544-7 Title: Perfect score:

114 1 KLGFFAHKKIPEEEKREEKLEQ 22 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1418010 segs, 331997259 residues Searched:

306921 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 22

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 67, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 15, Appl	Sequence 15, Appl		Sequence 1855, Ap	Sequence 36284, A					
QI	3 US-10-101-487-67	US-09-320-907B-24	US-10-447-292-24	US-09-320-907B-15	US-10-447-292-15	US-10-786-505-26	US-09-736-457-1855	US-09-902-941-1855	US-09-849-626-1855	US-10-017-754-1855	US-10-113-872-1855	US-10-283-017-1855	US-09-864-761-36284.
98	13	0	15	σ	15	16	σ	σ	σ	14	14	12	σ
% Query Match Length DB	19	20	20	20	20	16	20	20	20	20	20	20	22
Query Match	38.6	38.6	38.6	37.7	37.7	36.8	34.2	34.2	34.2	34.2	34.2	34.2	33.3
Score	44	44	44	43	43	42	39	39	39	39	39	39	38
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Sequence 1856, Ap Sequence 100, App Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 118, Appl Sequence 118, Appl Sequence 119, Appl Sequence 110, Appl Sequence 100, Appl Sequence 100, Appl Sequence 1, Appl Sequence 21, Appl	ก็ผู้ที่ผู้ที่เกิด
9 US-09-736-457-1856 9 US-09-902-941-1856 9 US-09-849-626-1856 14 US-10-017-754-1856 15 US-09-876-904A-510 16 US-09-876-904A-510 17 US-09-733-179A-5 18 US-09-733-179A-5 19 US-09-733-179A-15 10 US-09-733-179A-15 10 US-09-733-179A-15 10 US-09-733-179A-15 10 US-09-733-179A-15 10 US-09-733-179A-16 11 US-10-978-16 12 US-10-350-10 13 US-10-950-010-10 15 US-10-950-010-10 17 US-10-950-010-10 18 US-09-880-149-1 19 US-09-880-149-1 19 US-09-880-149-1 19 US-09-880-149-1	14 US-10-345-281-1 14 US-10-057-789-231 14 US-10-1212-628-231 14 US-10-177-550-5 14 US-10-177-550-26 9 US-09-320-907B-25 15 US-10-447-292-25
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ALIGNMENTS

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APPLICANT: BERGRAN, PHILIP A.
APPLICANT: BERGRAN, PHILIP A.
APPLICANT: BERGRAN, PHILIP A.
APPLICANT: BERGRAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT FILING DATE: 2002-03-20
PRIOR PLICATION NUMBER: 60/277,705
PRIOR PLICATION DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 67
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide US-10-101-487-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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; Sequence 67, Application US/10101487; Publication No. US20020169125A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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9 KIPEEEKREEKLEQ 22 |:||||: ||: |: KMPEEEEEEEEEE 15 N ò ద

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Sequence 26, Application US/10786505; Publication No. US20050003388A1; GENERAL INFORMATION:
A PAPLICANT: GROSS, RICHARD W.
APPLICANT: DAVID J. MANCUSO;
TITLE OF INVENTION: CALCIUM INDEPENDENT PHOSPHOLIPASE A2Y POLYNUCLEOTIDES;
TITLE OF INVENTION: AND POLYPEPTIDES AND METHODS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20030224453A1

Sequence 15, Application US/10447292

Publication No. US20030224453A1

GENERAL INPORMATION:

APPLICANT: PFAFF, MARTIN

TITLE OF INVENITON: TRANSMEMBRANE RECEPTORS

TITLE OF INVENITON: TRANSMEMBRANE RECEPTORS

FILE REFERENCE: SRI-0006

CURRENT APPLICATION NUMBER: US/10/447,292

CURRENT FILING DATE: 1999-05-27

PRIOR FILING DATE: 1999-05-27

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATCHTION VET: 2.00

SEQ ID NO 15

LEMUTH: 200

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                                                                                         APPLICANT: PFAFF, MARTIN

TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF

TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS

FILE OF INVENTION: TRANSMEMBRANE RECEPTORS

FILE OF INVENTION: 1806

CURRENT APPLICATION NUMBER: US/09/320,907B

CURRENT APPLICATION NUMBER: US/09/320,907B

PRIOR APPLICATION NUMBER: 09/187,236

PRIOR APPLICATION NUMBER: 09/187,236

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PALENTH VEY: 2.0

SEQ ID NO 15

LENGTH: 20
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-320-907B-15
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US-10-447-292-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.7%; Score 43; DB 9; Length 20; Best Local Similarity 50.0%; Pred. No. 57; Matches 9; Conservative 2; Mismatches 7; Indels
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ORGANISM: Artificial Sequence
                                               APPLICANT: GINSBERG, MARK H.
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-786-505-26
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                                                                                                   Sequence 24, Application US/09320907B
FUDILCALL INFORMATION:
APPLICANT: 0220020198360A1
GENERAL INFORMATION:
APPLICANT: GINSBERG, MARK H.
APPLICANT: GINSBERG, MARK H.
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE REPERENCE: SRI-0006
CURRENT PAPLICATION NUMBER: US/09/320,907B
CURRENT FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR FILING DATE: 1998-11-05
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
CHARLING DATE: D
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TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF

TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS

FILE REFERENCE: SRI-0006

CURRENT APPLICATION NUMBER: US/10/447,292

CURRENT APPLICATION NUMBER: US/09/320,907B

PRIOR APPLICATION NUMBER: US/09/320,907B

PRIOR PILING DATE: 1999-02-27

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 24

LENGTH: 20
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US-10-447-292-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Seguence:Synthetic
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38.6%; Score 44; DB 15; Length 20;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 7; Indels
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38.6%; Score 44; DB 9; Length 20;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 7; Indels
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8-09-320-907B-15
1 Sequence 15, Application US/09320907B
1 Publication No. US20020198360A1
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Publication No. US20030224453A1
GENERAL INFORMATION:
APPLICANT: GINSBERG, MARK H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLGFFAHKKIPEEEKREE 18
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ORGANISM: Artificial Sequence
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                                                                                   US-09-320-907B-24
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Sequence 1865, Application Wood 1969A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Wang, Aljun
APPLICANT: Wang, Tongtong
APPLICANT: Money Tongtong
APPLICANT: Money Tongtong
APPLICANT: Money Tongtong
TAPLICANT: Money Tongtong
TAPLICANT: Money Tongtong
TITLE OF INVENTION: DIACONSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIACONSIS OF LUNG CANCER
TITLE OF INVENTION: DIACONSIS OF LUNG CANCER
TILLE REPERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
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                                                       APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 39; DB 9; 53.8%; Pred. No. 2e+02;
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Pred. No. 2e+02;
3; Mismatches
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Publication No. US20030054363A1
GENERAL INFORMATION:
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Carter, Darrick
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
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53.8%;
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Best Local Similarity 53.0.
Best Local 7; Conservative
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Best Local Similarity 53.0.
Best Tocal 7; Conservative
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8 ARKKVEEEDEEEE 20
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ARKKVEEEDEEEE 20
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1855
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US-09-849-626-1855
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CURRENT APPLICATION NUMBER: US/09/736,457
                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide
US-10-786-505-26
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Pred. No. 2e+02;
3; Mismatches 3; Indels
; FILE REFERENCE: 15060-58
; CURRENT APPLICATION NUMBER: US/10/786,505
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: 09/168,623
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 26
; LENGTH: 16
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Patent No. US20020168637A1
PAPERAL INFORMATION:
APPLICANT: Wang, Tongtong
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Patent No. US20020172952A1
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Bangur, Chaitanya S.
Lodes, Michael A.
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ORGANISM: Artificial Sequence
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2 ENIPLDESRNEKLDQ 16
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Best Local Similarity 53.0-
T. Conservative
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8 ARKKVEEEDEEEE 20
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; ORGANISM: Homo sapiens
US-09-736-457-1855
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Darrick
                         Fanger, G
Vedvick,
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APPLICANT: Macdiade, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Stath, Paul R.
APPLICANT: Stath, Paul R.
APPLICANT: Garter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT PILLING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
ISSQ ID NO 1855
             APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
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llarity 53.8%; Pred. No. 2e+02;
Conservative 3; Mismatches 3; Indels
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Pred. No. 2e+02;
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Sequence 1855, Application US/10283017
Publication No. US20030211510A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Butter, Marc W.
APPLICANT: Durham, Margarita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1855, Application US/10113872
Publication No. US20030170255A1
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro
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Best Local Similarity 53.8:
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8 ARKKVEEEDEEEE 20
Fanger, Gary R.
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ORGANISM: Homo sapiens
US-10-017-754-1855
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 7; Conserv
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US-09-864-761-36284

Sequence 36284, Application US/09864761

Patent No. US20020048763A1

Patent No. US20020048763A1

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUMBER: US 60/180, 312

PRIOR PLILOM DATE: 2000-02-04

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-06-30

PRIOR PLILNG DATE: 2000-01-00

PRIOR PLILNG DATE: 2000-01-00

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30
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Pred. No. 2e+02;
3; Mismatches 3; Indels
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
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FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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Thomas S.
Chaitanya S.
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Best Local Similarity 53.0%
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8 ARKKVEEEDEEEE 20
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ORGANISM: Homo sapiens
US-10-283-017-1855
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Search completed: April 6, 2005, 15:11:37 Job time : 138 secs
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APPLICANT: Bangur, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Bangur, Gary
APPLICANT: Farger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Reter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121478615
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SSOTION: 1856
SSOTION: 1856
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CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
US-09-864-761-36284
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33.3%; Score 38; DB 9; Length 22;
Best Local Similarity 61.5%; Pred. No. 2.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35284
LENGTH: 22
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Patent No. US20020168637A1
GENERAL INFORMATION:
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Patent No. US20020172952A1
GENERAL INFORMATION:
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Matches 6; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-736-457-1856
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Gaps
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APPLICANT: Faulet, Carl, Formas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE REPERBENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 20
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40.0%; Pred. No. 3.6e+02;
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US-09-902-941-1856
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Patent No. 5225193
Patent No. 5225193
Sequence 1856, Ap
Patent No. 5225193
Patent No. 5225193
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                                                                                                  2005, 14:50:40 ; Search time 43 Seconds (without alignments) 38.193 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-127-499A-15
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US-08-554-616-25
US-09-515-965A-1640
US-09-350-841A-1669
US-10-073-028-24
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US-08-554-616-24
US-09-515-965A-1641
US-09-350-841A-1670
US-09-350-841A-1670
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US-09-736-457-1855
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US-08-690-011A-4
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1 KLGFFAHKKIPBEEKREEKLEQ 22
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Maximum Match 100%
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length: 22
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Maximum DB seq
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wuwww444wuuww44w4	Mark H. Tim Mark H. Tim METHODS FOR METHODS FOR 19 S: Richardson in Street ts Model 502 MS-003 (Versio ATA: US/08/214 US/08/214 T. T. 30,162 MBATION: T. 30,162 MBATION: 42-5070 -8906 -8906 -8006 -8906	
2000 2000 2011 2011 2011 2011 2011	US ALL TITULE OR THE TREE OR T	37.7%; 50.0%; tive
	LT 1 quence 1, Application US/ tent No. 5523209 tent No. 5523209 APPLICANT: Ginsberg, Ma APPLICANT: Ginsberg, Ma TITLE OF INVENTION: MET TITLE OF INVENTION: MET TITLE OF INVENTION: INH TITLE OF INVENTION: ACT TOWNERS: MOSA COUNTRY: U.S.A. ZIP: MASSACHUSELE FORM: MEDIUM TYPE: 3.5" Dis COMPUTER: IBM PS/2 MO OPERATING SYSTEM: MS- SOFTWARE: WORDPERFECT CUASSIFICATION NUMBER: TILING DATE: CLASSIFICATION NUMBER: ATTORNEY/AGENT INFORMATI NAME: CLARK, PAUL T. REGISTRATION NUMBER: TELEPHONE: (617) 542-89 TELESA: (617) 5	37. larity 50. Conservative
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00000000000000000000000000000000000000	RESULT 1 Sequence 1, Application Sequence 1, Application Batent No. 5523209 GENERAL INFORMATION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: Fish & STRREET: 225 Frankl CITY: Boston STATE: Massachuset COUNTRY: U.S.A. ZILL 02110-2804 COMPUTER: IBM PS/2 COMPUTER: IBM PS/2 COMPUTER: IBM PS/2 COMPUTER: MACHELCATION NUMBER: FILLING DATE: CURRENT APPLICATION DATE: CURRENT APPLICATION DATE: CURRENT APPLICATION DATE: TILLING DATE: T	Query Match Best Local S Matches
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Gaps
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICATION: BARTPAL, TAMAS
TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION UNDER: 18507/346,837
FILING DATE: 19-OCT-1987
                                                                                                                                                                                                                                                                                                                                       Length 20;
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37.7%; Score 43; DB 5;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                       # MOLECULE TYPE: peptide
| HYPOTHETICAL: NO | FRAGMENT TYPE: C-terminal | ORIGINAL SOURCE: | ORGANISM: Homo sapiens integrin alpha-IIb | PCT-US95-07542-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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FILING DATE: 13-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-JUN-1994
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1855, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
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Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity 53.0.
The Conservative 7; Conservative
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                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepti
HYPOTHETICAL: NO
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LENGTH: 20
TYPE: PRT
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APPLICANT:
APPLICANT:
APPLICANT:
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5225193-7
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                                                                                                                                        Sequence 1, Application PC/TUS9502885
GENERAL INFORMATION:
APPLICANT: Ginaberg, Mark H.
APPLICANT: Ginaberg, Timothy
TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
TITLE OF INVENTION: OF INTEGRIN ACTIVATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTINE Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,770
FILING DATE: March 14, 1994
ATTORNEY, AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06410/002001
TELECHONE (617) 542-5070
TELEPHONE: (617) 542-5070
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// GENERAL INFORMATION:
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  1 KLGFFAHKKIPEEEKREE 18
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Best Local Similarity 50.0°
Matches 9; Conservative
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , TOPOLOGY:
PCT-US95-02885-1
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Score 36; DB 6; I
Pred. No. 1.3e+02;
3; Mismatches 4;
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Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                              SEQ ID NO:2:
; LENGTH: 20
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LENGTH: 20
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APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION NUMBER: US/09/736,457
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                          Patent No. 5225193
PAPLICATION: BARTFAL, TAMAS
TITLE OF INVENTION: BONDETELLA TOXIN PEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/346,837
FILING DATE: 19-OCT-1987
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95;
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Pred. No. 51;
5; Mismatches 8; Indels
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 DB 6; Length 20;
                                 8; Indels
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Pred. No. 95;
6; Mismatches
 Score 39; DB
Pred. No. 51;
5; Mismatches
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1 KSEYLAHRRIPPENIRTRV 20
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Bangur, Chaitanya S.
Lodes, Michael A.
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Best Local Similarity 35.0%;
Matches 7; Conservative
Query Match
Best Local Similarity 35.0%;
Matches 7; Conservative
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KKVEEEDEEQEEEEE 16
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserva
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;Patent No. 5225193
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SEQ ID NO:7:
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LENGTH: 20
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LENGTH: 20
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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; Sequence 25, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
    APPLICANT: Bolognesi, Dani P.
    APPLICANT: Matthews, Thomas J.
    APPLICANT: Wild, Carl T.
    TITLE OF INVENTION: SYNTHERIC PEPTIDE INHIBITORS OF HIV TITLE OF INVENTION: TRANSMISSION
    VUMBER OF SEQUENCES: TANSMISSION
    NUMBER OF SEQUENCES: TANSMISSION
    NUMBER OF SEQUENCES: A CORRESPONDENCE ADDRESS:
    ATREET: 1155 Avenue of the Americas
    CITY: New York
    CORRESPONDENCE ADDRESS:
    ATREET: New York
    CORRESPONDENCE ADDRESS:
    ATREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5225193-2
;Patent No. 5225193
TTLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
TITLE OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/346,837
FILING DATE: 19-OCT-1987
APPLICANT: BARTFAI, TAMAS
TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/346,837
FILING DATE: 19-OCT-1987
                                                                                                                                                                                                                                                                              Score 36; DB 6; Length 20;
Pred. No. 1.3e+02;
3; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
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D.C.
    ; Patent No. 5556757
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PACENT NO. 5510264
GENERAL INFORMATION:
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 & Street, N.W., Suite 500
CITY: Mashington
                                                                                                                                                                                                               Query Match 31.6%; Score 36; DB 1; Length 21; Best Local Similarity 43.8%; Pred. No. 1.4e+02; Matches 7; Conservative 3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REPERENCE/DOCKET NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION NUMBER: 51916/102/INBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 1.4e+02;
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43.8%; Pred. No. 1.4e+02
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15, Application US/08482847
                TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
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                                                                                                                                                                                                                                                                                             7 HKKIPEEEKREEKLEQ 22
(212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 43.0-
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                              / MOLECULE TYPE: peptide
US-08-073-028-25
                                                                                                                    TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , TOPOLOGY:
US-08-127-499A-15
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                          US-08-127-499A-15
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US-08-482-847-15
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PEPTIDES RÉPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mitchews, Thomas J.
APPLICANT: Wild. Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
TOWNESS OF SEQUENCES: 74
CORRESPONDENCES. Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IDPOPY disk
COMPUTER: IDPOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: US/09/482,847
FILING DATE: US/09/482,847
PRIOR APPLICATION NUMBER: US/08/127,499
FILING DATE: 28-SEP-1993
ATTONREY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5399
                                                                       TITLE OF INVENTION: PEPTIDES REPRESENTING TITLE OF INVENTION: BACTERIAL AND VIRAL MITHLE OF INVENTION: CNS CARRIER, ANTIBODI NUMBER OF SEQUENCES:
ADDRESSEE: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08554616; Patent No. 6133418; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
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Best Local Similarity
Matches 7; Conserv
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FEATURE:
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APPLICANT: Erickson, J.
APPLICANT: Erickson, J.
APPLICANT: Extekson, J.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REPERRINGE: 7872-073
CURRENT APPLICATION NUMBER: 09/915,965A
CURRENT APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FESTERE for Windows Version 3.0
SEQ ID NO 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.6%; Score 36; DB 3; Length 21; 43.8%; Pred. No. 1.4e+02; tive 3; Mismatches 6; Indels
                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION DATA:
RPPLICATION DATA:
APPLICATION DATA:
RPPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
RELEPAN: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 700-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1640, Application US/09515965A
Patent No. 6623741
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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HSLIEESQNQQEKNEQ 21
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Best Local Similarity 43.8°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-09-515-965A-1640
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Search completed: Application US/09350841A

Search completed: 1669, Application US/09350841A

Patent No. 6750008

General INFORMATION:
APPLICANT: Jeffs, Peter;
TITLE OF INVENTION:
FILE REFERENCE: 702-06-99

CURRENT FILING DATE: 1999-07-09

CURRENT FILING DATE: 2.1

TYPE: PRT

CURRENT FILING DATE: 1999-07-09

CURRENT FILING DATE:
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